

76496

From: Mertz, Prema  
Sent: Wednesday, September 25, 2002 2:48 PM  
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Please search SEQ ID NO:1, 3, wit DNA databases.

Please searc SEQ ID NO:2, 4 with protein databases.

Thanks

Prema Mertz, Ph.D.  
Primary Examiner  
Art Unit 1646  
Crystal Mall 1, Room 10E-01  
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CREF

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 9/26/02  
Date Completed: 9/29/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: 2  
AA Sequences: 2  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 86  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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DEFINITION	Sequence 8 from patent US 5747033.		
ACCESSION	AR004292		
VERSION	AR004292.1 GI:3965171		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1070)		
AUTHORS	Davis, S., Gale, N.W., Aldrich, T.H., Maisonnier, P.C., Goldfarb, M., and Vancopoulos, G.D.		
TITLE	Method of enhancing the biological activity of Eph family ligands		
JOURNAL	Patent: US 5747033-A 8 05-MAY-1998;		
FEATURES	Location/Qualifiers		
source	1..1070		
BASE COUNT	196 a 341 c 334 g 189 t		10 others
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QY	785	TTCTTGCCCTCTAGCTCTGCCCTCCCTCGGGGGGAGAGATGGGC	834
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RESULT	9		
LOCUS	AC021890		
DEFINITION	Homo sapiens chromosome 3 clone RP11-498A2, WORKING DRAFT SEQUENCE,	175826 bp	DNA linear
ACCESSION	AC021890	22 unordered clones.	
VERSION	AC021890.12	GI:11128300	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Plrimates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 175826)		
	Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaraturge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowles, S., Brieve, M., Brown, M., Bryant, N.P., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Huly, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louissegh, R., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, S., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williams, A., Wlezyk, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D. and Gibbs, R.		

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Direct Submission  
Unpublished  
2 (bases 1 to 175826)  
Worley, K.C.  
Direct Submission  
Submitted (22-JAN-2000) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Nov 9, 2000 this sequence version replaced gi:9719697.  
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Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
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Project Information  
Center project name: HMZE  
Center clone name: RP11-498A2  
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Summary Statistics  
Sequencing vector: M13; L08821  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 144734 bases at least Q40  
Consensus quality: 162873 bases at least Q30  
Consensus quality: 169424 bases at least Q20  
Estimated insert size: 170770; sum-of-coverage estimation  
Quality coverage: 0x in Q20 bases; agarose-fp estimation  
Quality coverage: 3.3x in Q20 bases; sum-of-coverage estimation

COMMENT

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NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
NOTE: This is a 'working draft' sequence. It currently  
consists of 22 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.  
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Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Db 39098 GAAGACTTTGAGGGAGAGAACCTCAGGTGCCCAAGCTTGAGAGAGCATCAGCGGACC 39157  
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LOCUS AB051678 1838 bp mRNA linear VRT 20-SEP-2001  
DEFINITION Danio rerio mRNA for ephrin-A3, complete cds.  
ACCESSION AB051678  
VERSION AB051678.1 GI:14196230  
KEYWORDS  
SOURCE Danio rerio cDNA to mRNA.  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE  
AUTHORS Hirate, Y., Mieda, M., Harada, T., Yamasu, K. and Okamoto, H.  
TITLE Identification of ephrin-A3 and novel genes specific to the  
midbrain-MHB in embryonic zebrafish by ordered differential display  
Mechanisms of development. 107 (1-2), 83-96 (2001)  
JOURNAL 21412237  
MEDLINE 2 (bases 1 to 1838)  
REFERENCE Hirate, Y., Mieda, M., Harada, T., Yamasu, K. and Okamoto, H.  
AUTHORS Direct Submission  
TITLE Submitted (24-NOV-2000) Yoshikazu Hirate, Brain Science Institute,  
RIKEN, Lab. of Developmental Gene Regulation; 2-1, Hirosawa,  
Wako-shi, Saitama 351-0198, Japan (E-mail:hirate@brain.riken.go.jp,  
Tel:81-48-467-9713, Fax:81-48-467-9714)  
FEATURES  
Location/Qualifiers

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ORIGIN

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Qy 175 CCGCATCGCGGTACTGGACACCTCCACACGACCTCGCGGAGAGGGCTACACGT 234
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Qy 355 GAGCCGCACCGGTACCGACCTCGACAGCCAGCGGCTTCAGCGCTGGAGTGAA 414
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RESULT 11
LOCUS AY045577
DEFINITION Rattus norvegicus ephrin A3 mRNA, linear
ACCESSION AY045577
VERSION AY045577.1 GI:15290522
KEYWORDS Norway rat.

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 355)
Munoz,J.J., Alonso-C,L.M., Sacedon,R., Crompton,T., Vicente,A.,
Jimenez,E., Varas,A. and Zapata,A.G.
Expression and function of the Eph A receptors and their ligands
ephrens A in the rat thymus
Unpublished
2 (bases 1 to 355)
Munoz,J.J., Alonso-C,L.M., Sacedon,R., Crompton,T., Vicente,A.,
Jimenez,E., Varas,A. and Zapata,A.G.
Direct Submission
Submitted (13-JUL-2001) Cell Biology, Complutense University of
Madrid, Av. Complutense, Madrid 28040, Spain
FEATURES
source
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Db 200 AATTCCATGCGGCGGAGATACTACTATCTCCAGCGGCTACACACCTGCACTGGA 259
Qy 552 AGTGTCTGAGGATGAAGGTTCGTCTGCTGCGCTCCACATCGCACTCCGCGGAGAGC 611
Db 260 AGTGTCTGAGGATGAAGGTTCGTCTGCTGCGCTCCACAACTTTGAGGAGAGAAATC 319
Qy 612 C 612
Db 320 C 320

RESULT 12
LOCUS U92885
DEFINITION Mus musculus LERK-3 (Epl3) gene, partial cds.
ACCESSION U92885
VERSION U92885.1 GI:2843098
KEYWORDS house mouse.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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87207 90387: contig of 3180 bp in length
90387 90487: gap of unknown length
90487 92854: contig of 2367 bp in length
92854 92954: gap of unknown length
92954 96442: contig of 3488 bp in length
96442 98997: gap of unknown length
98997 99097: gap of unknown length
99097 102593: contig of 3496 bp in length
102593 102693: gap of unknown length
102693 105584: contig of 2891 bp in length
105584 105684: gap of unknown length
105684 108442: contig of 2758 bp in length
108442 108542: gap of unknown length
108542 111917: contig of 3375 bp in length
111917 112017: gap of unknown length
112017 116076: contig of 4059 bp in length
116076 116176: gap of unknown length
116176 119383: contig of 3207 bp in length
119383 119483: gap of unknown length
119483 123902: contig of 4419 bp in length
123902 124002: gap of unknown length
124002 127609: contig of 3607 bp in length
127609 131621: contig of 3912 bp in length
131621 131721: gap of unknown length
131721 135933: contig of 4212 bp in length
135933 136033: gap of unknown length
136033 140801: contig of 4768 bp in length
140801 140901: gap of unknown length
140901 144622: contig of 3721 bp in length
144622 144722: gap of unknown length
144722 148869: contig of 4147 bp in length
148869 148870: gap of unknown length
148870 153203: contig of 4234 bp in length
153203 153303: gap of unknown length

```

```

153304 157194: contig of 3891 bp in length
157194 157294: gap of unknown length
157294 162013: contig of 4719 bp in length
162013 162113: gap of unknown length
162113 167799: contig of 5686 bp in length
167799 167899: gap of unknown length
167899 173081: contig of 5182 bp in length
173081 173181: gap of unknown length
173181 180558: contig of 7377 bp in length
180558 180658: gap of unknown length
180658 186794: contig of 6136 bp in length
186794 186894: gap of unknown length
186894 192068: contig of 5174 bp in length
192068 192168: gap of unknown length
192168 198394: contig of 6226 bp in length
198394 198494: gap of unknown length
198494 203084: contig of 4590 bp in length
203084 203184: gap of unknown length
203184 208688: contig of 5504 bp in length
208688 208788: gap of unknown length
208788 214457: contig of 5669 bp in length
214457 214557: gap of unknown length
214557 219456: contig of 4899 bp in length
219456 219556: gap of unknown length
219556 226019: contig of 6463 bp in length
226019 226119: gap of unknown length
226119 234001: contig of 7882 bp in length
234001 234101: gap of unknown length
234101 241495: contig of 7398 bp in length
241495 241599: gap of unknown length
241599 249134: contig of 7535 bp in length
249134 249234: gap of unknown length
249234 259781: contig of 10547 bp in length
259781 259881: gap of unknown length
259881 267444: contig of 7563 bp in length
267444 267544: gap of unknown length
267544 279432: contig of 11888 bp in length
279432 279532: gap of unknown length
279532 279533: contig of 10047 bp in length.

```

## FEATURES

## SOURCE

```

1. 289579
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="rp23-368d24"
/clone_lib="rPCI mouse BAC library 23"

```

```

BASE COUNT 70974 a 71815 c 70765 g 58626 t 7399 others
ORIGIN

```

```

Query Match 21.4% Score 222; DB 2; Length 289579;
Best Local Similarity 84.7% Pred. No. 1.2e-25;
Matches 271; Conservative 0; Mismatches 25; Indels 24; Gaps 1;

QY 205 CCAGCAGCTGGCGGAGAGGCTACCGTGAGTGAACTGACGACTACTCTGGATAT 264
|||||
Db 185995 CCACAGCCTGGCGGAGAGGCTACCGTGAGTGAACTGACGACTACTCTGGATAT 185936
|||||

QY 265 TTACTGCCGCACCTACACAGCTCGGGGTGGCCCCGGGGGAGG 324
|||||
Db 185935 TTACTGCCGCACCTACACAGCTCGGGGTGGCCCCGGGGGAGG 185900
|||||

QY 325 CGGGCAGCAGCAGTACGCTGCTGATGATGAGCGGCAACGCTACCGCAGCTGCAAGCC 384
|||||
Db 185899 CGGGCAGCAGCAGTACGCTGCTGATGATGAGCGGCAACGCTACCGCAGCTGCAAGCC 185840
|||||

QY 385 CAGCCAGGCTTCAAGCGCTGGGAGTGCACCGCGCCGACCGCCGACAGCCCATCAA 444
|||||
Db 185839 CAGCCAGGCTTCAAGCGCTGGGAGTGCACCGCGCCGACCGCCGACAGCCCATCAA 185780
|||||

QY 445 GTTCTCGGAGAGTTCACAGCGCTACAGCGCTTCTCTCTGGGCTACGAGTTCACGCGCGG 504
|||||
Db 185779 GTTCTCGGAGAGTTCACAGCGCTTCTCTCTGGGCTACGAGTTCACGAGTTCATGATTCACGCGG 185720
|||||

```

OY 505 CCACGAGTACTACTACTACT 524  
LOCUS ||| || ||||| ||||| |||||  
Db 185719 CCAAGAATACTACTACTACT 185700

RESULT 14  
AC104327 326750 bp DNA linear HTG 24-DEC-2001  
LOCUS Mus musculus clone rp23-295a4 strain C57BL/6J, WORKING DRAFT  
DEFINITION SEQUENCE, 66 unordered pieces.  
ACCESSION AC104327  
VERSION AC104327.2 GI:17978117  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 326750)  
Hua, A. and Roe, B. A.  
Mus musculus BAC Clone rp23-295a4  
Unpublished  
2 (bases 1 to 326750)  
Hua, A. and Roe, B. A.  
Direct Submission  
Submitted (10-DEC-2001) Department of Chemistry And Biochemistry,  
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
On Dec 24, 2001 this sequence version replaced gi:17439220.  
----- Genome Center  
Center: Department of Chemistry And Biochemistry  
The University of Oklahoma  
Center code: UOKNOR  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 66 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 2180: contig of 2180 bp in length  
\* 2181 2280: gap of unknown length  
\* 2281 4455: contig of 2175 bp in length  
\* 4456 4555: gap of unknown length  
\* 4556 7347: contig of 2792 bp in length  
\* 7348 7447: gap of unknown length  
\* 7448 10057: contig of 2610 bp in length  
\* 10058 10157: gap of unknown length  
\* 10158 12254: contig of 2097 bp in length  
\* 12255 12354: gap of unknown length  
\* 12355 14417: contig of 2063 bp in length  
\* 14418 14517: gap of unknown length  
\* 14518 18079: contig of 3562 bp in length  
\* 18080 18179: gap of unknown length  
\* 18180 20239: contig of 2060 bp in length  
\* 20240 20339: gap of unknown length  
\* 20340 22342: contig of 2003 bp in length  
\* 22343 22442: gap of unknown length  
\* 22443 24502: contig of 2060 bp in length  
\* 24503 24602: gap of unknown length  
\* 24603 26620: contig of 2018 bp in length  
\* 26621 28720: gap of unknown length  
\* 28721 30776: contig of 4056 bp in length  
\* 30777 30877: gap of unknown length  
\* 30877 33188: contig of 2312 bp in length  
\* 33189 33288: gap of unknown length  
\* 33289 36016: contig of 2728 bp in length  
\* 36017 38116: gap of unknown length  
\* 38117 38176: contig of 2060 bp in length  
\* 38177 38276: gap of unknown length  
\* 38277 40782: contig of 2506 bp in length

40783 40882: gap of unknown length  
40883 43672: contig of 2790 bp in length  
43673 43772: gap of unknown length  
43773 46580: contig of 2808 bp in length  
46581 46680: gap of unknown length  
46681 49679: contig of 2999 bp in length  
49680 49779: gap of unknown length  
49780 52528: contig of 2749 bp in length  
52529 52628: gap of unknown length  
52629 56785: contig of 4157 bp in length  
56786 56885: gap of unknown length  
56886 59118: contig of 2233 bp in length  
59119 62964: contig of 3746 bp in length  
62965 63064: gap of unknown length  
63065 65910: contig of 2846 bp in length  
65911 66010: gap of unknown length  
66011 69396: contig of 3386 bp in length  
69397 69496: gap of unknown length  
69497 72554: contig of 3058 bp in length  
72555 72654: gap of unknown length  
72655 75720: contig of 3066 bp in length  
75721 75820: gap of unknown length  
75821 79364: contig of 3544 bp in length  
79365 79464: gap of unknown length  
79465 82699: contig of 3135 bp in length  
82699 82997: contig of 2598 bp in length  
82998 85397: gap of unknown length  
85398 89123: contig of 3726 bp in length  
89124 89223: gap of unknown length  
89224 92441: contig of 3218 bp in length  
92442 92542: gap of unknown length  
92543 95856: contig of 3315 bp in length  
95857 95956: gap of unknown length  
95957 99508: contig of 3552 bp in length  
99509 103789: gap of unknown length  
103789 103889: contig of 4181 bp in length  
103890 109457: contig of 5568 bp in length  
109458 109557: gap of unknown length  
109558 114011: contig of 4454 bp in length  
114012 114111: gap of unknown length  
114112 116551: contig of 4540 bp in length  
116552 118751: gap of unknown length  
118752 123608: contig of 4857 bp in length  
123609 123708: gap of unknown length  
123709 127713: contig of 4005 bp in length  
127714 127813: gap of unknown length  
127814 133303: contig of 5490 bp in length  
133304 133403: gap of unknown length  
133404 136767: contig of 3364 bp in length  
136768 136867: gap of unknown length  
136868 142660: contig of 5793 bp in length  
142661 142760: gap of unknown length  
142761 146700: contig of 3940 bp in length  
146701 146800: gap of unknown length  
146801 151040: contig of 4240 bp in length  
151041 151141: gap of unknown length  
151142 155319: contig of 4179 bp in length  
155320 155419: gap of unknown length  
155420 159447: contig of 4028 bp in length  
159448 159547: gap of unknown length  
159548 163961: contig of 4414 bp in length  
163962 164061: gap of unknown length  
164062 169232: contig of 5171 bp in length  
169233 169332: gap of unknown length  
169333 173172: contig of 3840 bp in length  
173173 173272: gap of unknown length  
173273 178980: contig of 5708 bp in length  
178981 179080: gap of unknown length  
179081 188181: contig of 9101 bp in length  
188182 188281: gap of unknown length

```

* 188282 192848: contig of 4567 bp in length
* 192849 192948: gap of unknown length
* 192949 198249: contig of 5301 bp in length
* 198250 198349: gap of unknown length
* 198350 206031: contig of 7682 bp in length
* 206032 206131: gap of unknown length
* 206132 210282: contig of 4151 bp in length
* 210283 218415: contig of 8033 bp in length
* 218416 218515: gap of unknown length
* 218516 226120: contig of 7605 bp in length
* 226121 226220: gap of unknown length
* 226221 236580: contig of 10360 bp in length
* 236581 236680: gap of unknown length
* 236681 245273: contig of 8593 bp in length
* 245274 245373: gap of unknown length
* 245374 256115: contig of 10742 bp in length
* 256116 256215: gap of unknown length
* 256216 264078: contig of 7863 bp in length
* 264079 273637: contig of 9459 bp in length
* 273638 273737: gap of unknown length
* 273738 295230: contig of 21493 bp in length
* 295231 295330: gap of unknown length
* 295331 313298: contig of 17968 bp in length
* 313299 313399: gap of unknown length
* 313399 326750: contig of 13352 bp in length.

```

## FEATURES

```

1..326750
    source
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone_lib="rp23-295a4"
        /clone_lib="RPCI mouse BAC library 23"
BASE COUNT 79344 a 80488 c 78974 g 81219 t 6725 others
ORIGIN

```

```

Query Match      21.4%; Score 222; DB 2; Length 326750;
Best Local Similarity 84.7%; Pred. No. 1.2e-25;
Matches 271; Conservative 0; Mismatches 25; Indels 24; Gaps 1;

```

```

QY 205 CCAGCACCCTCGGGGAGAGGGCTACACCGTGCAGGTGAAGTGAACGACATCTGGATAT 264
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 194171 CCACAGCCTCGGGGAGAGGGCTACACCGTGCAGGTGAAGTGAACGACATCTGGATAT 194230
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 265 TTACTGCCCACTTACAAACAGCTCGGGGGTGGCCCGGGGGGACCGCCGGGAGG 324
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 194231 TTACTGCCCACTTACAAACAGCT-----CAGGGCTTGGCGG 194266
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 325 CGGGGAGAGCAGTACGTGTGTACATGTGTAGCGCGGACCGGTACCGCACCTGCAACGC 384
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 194267 CGGGGAGAGCAGTACGTGTGTGTACATGTGTAGCGCGGTACCGCACCTGCAACGC 194326
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 385 CAGCAGGGCTTCAAGCGCTGGAGTGCAACCGCGCGCAGCCCGGCACAGCCCCATCAA 444
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 194327 CAGCAGGGCTTCAAGCGCTGGGAATGCAACCGCGCAGCCCTGCGCACAGCCCCATCAA 194386
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 445 GTTCTCGGAAGTTCACAGCGCTACAGCGCTTCTCTCTGGGCTACAGTTCACAGCCGG 504
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 194387 GTTCTCGGAAGTTCACAGCGCTTCTCTCTGGGCTACAGTTCATGATTCATGCGCG 194446
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 505 CCACGAGTACTACTATCT 524
      ||| || ||||| ||||| |||||
Db 194447 CCAGAATACTACTATCT 194466

```

## RESULT 15

```

AC104632 AC104632 289579 bp DNA linear HTG 29-DEC-2001
LOCUS Mus musculus clone rp23-368d24 strain C57BL/6J, WORKING DRAFT
DEFINITION SEQUENCE, 72 unordered pieces.
ACCESSION AC104632

```

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AC104632.2 GI:17998594  
HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
house mouse.

## REFERENCE

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 21:19:25 ; Search time 239.05 Seconds  
(without alignments)  
7447.983 Million cell updates/sec

Title: US-09-904-954-1

Perfect score: 1037

Sequence: 1 GGATCTTGAACGAGACGAC.....GTGCTGTCGTTCCAGATCC 1037

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.\*  
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21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1037	100.0	1037	16	AA085887 Human hek-L protei
2	907.4	87.5	1070	16	AA0703883 Eph transmembrane
3	205.8	19.6	358	21	AA03424 Human secreted pro
4	151.8	14.6	642	20	AA032767 Human LERK-6 poly
5	149.2	14.4	783	17	AA015009 Chicken elf-1 cDNA
6	149.2	14.4	783	17	AA042927 cDNA encoding an a
7	149.2	14.4	1809	17	AA015008 Mouse Elf-1 cDNA.
8	149.2	14.4	1809	17	AA042926 cDNA encoding a ma
9	135.4	13.1	314	17	AA014010 LERK-6 exon. Homo

10	135.4	13.1	314	20	AA032766	Exon sequence of h
11	128.8	12.4	555	17	AA032700	Lerk-6 coding sequ
12	128.8	12.4	555	17	AA014009	Lerk-6 coding sequ
13	128.8	12.4	555	17	AA032761	Murine LERK-6 poly
14	116.4	11.2	1438	13	AA024595	B61 cDNA sequence.
15	116.4	11.2	1480	15	AA063770	B61 gene. Homo sa
16	116.4	11.2	1496	22	AA021387	Human cDNA sequenc
17	116.4	11.2	1496	22	AA090574	Human PRO202 cDNA.
18	116.4	11.2	1496	22	AA091576	Human PRO202 cDNA.
19	116.4	11.2	1527	21	AA098823	Human pancreatic c
20	114.8	11.1	439	22	AA081578	Human differential
21	108.6	10.5	1176	23	AA092024	DNA encoding novel
22	104	10.0	1574	23	AA092779	DNA encoding novel
23	104	10.0	1728	17	AA034292	HEK4 binding prote
24	104	10.0	1839	17	AA018897	Human AL-1 cDNA.
25	103.4	10.0	636	16	AA085888	Human hek-L protei
26	102	9.8	687	17	AA032699	Lerk-7 coding sequ
27	73.2	7.1	3066	23	AA075851	DNA encoding novel
28	58.8	5.7	1002	22	AA051628	Human polynucleoti
29	55.2	5.3	515	20	AA018930	Human huntingtin g
30	55.2	5.3	10348	20	AA023426	Human huntingtin p
31	55.2	5.3	10348	22	ABA08651	Human Huntingtin's
32	55.2	5.3	10348	23	AA091971	DNA encoding novel
33	55.2	5.3	10366	15	AA067401	Huntingtin DNA\Iti
34	55.2	5.3	10366	18	AA079924	Composite sequence
35	55.2	5.3	10366	19	AA050828	Human huntingtin c
36	54.8	5.3	645	17	AA042476	HuntL4 coding sequ
37	53.6	5.2	10348	22	ABA08714	Human Huntingtin's
38	52.6	5.1	3389	23	AA086290	DNA encoding novel
39	52	5.0	1059	20	AA072336	Actinomycete sp. 3
40	52	5.0	9732	23	AA079690	DNA encoding novel
41	51.2	4.9	270	20	AA037239	Seq ID No: 8 of WO
42	51.2	4.9	1924	22	AA059598	Human cell cycle a
43	50.6	4.9	255	22	AA082125	Rat differential t
44	50.2	4.8	1833	23	AB022159	Drosophila melanog
45	50.2	4.8	4403765	22	AA019683	Mycobacterium tube

#### ALIGNMENTS

RESULT 1	AA085887	standard; cDNA to mRNA; 1037 BP.
ID	AA085887	
XX	AC	AA085887;
XX	DT	03-OCT-1995 (first entry)
XX	DE	Human hek-L protein cDNA clone A2.
XX	KW	Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
KW	immunogen; ss.	
XX	OS	Homo sapiens.
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	83..799
FT		/*tag= a
FT	sig_peptide	83..139
FT		/*tag= b
FT	mat_peptide	140..796
FT		/*tag= c
XX		
PN	WO9506065-A.	
XX		
PD	02-MAR-1995.	
XX		
PF	17-AUG-1994;	94WO-US09282.
XX		
PR	20-AUG-1993;	93US-0109745.
PR	30-AUG-1993;	93US-011426.
PR	03-DEC-1993;	93US-0161132.

PR 09-MAY-1994; 94US-0240124.  
XX (IMV ) IMMUNEX CORP.  
PI Beckmann MP, Cerretti DP;  
XX WPI; 1995-106811/14.  
DR P-PSDB; AAR71481.  
XX New isolated DNA encoding hek-L protein or its fusion products -  
PT useful as assay reagent or for carrying therapeutic and  
PT diagnostic compounds to leukaemia cells.  
XX Claim 1; Page 34; 45pp; English.  
XX The sequence is that of a clone encoding hek-L protein, a protein  
CC that can bind hek (a cell surface receptor tyrosine kinase). Hek-L  
CC is the first known ligand for hek and can be used to study cellular  
CC processes regulated by hek (which may be involved in tumorigenesis).  
CC It is also an immunogen for antibody production, as a reagent for  
CC detecting hek or hek-L in in vitro assays, to determine binding of  
CC hek proteins, to purify hek proteins, and to carry diagnostic or  
CC cytotoxic agents to particular leukaemia cells that express the hek  
CC antigen. Hek-L also binds the elk tyrosine kinase receptors.  
CC See also AAQ85888.  
XX  
SQ Sequence 1037 BP; 187 A; 343 C; 337 G; 170 T; 0 other;

Query Match 100.0%; Score 1037; DB 16; Length 1037;  
Best Local Similarity 100.0%; Pred. No. 1.2e-186;  
Matches 1037; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ggetcttgaaacagacacactgctggagagccggagcgggctcagtcgggggc 60  
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DB 61 ggcgcgcgggcgggcgggatggcgggcgggctcgctgctgctgctgctgctgct 120  
QY 121 GCGCGTGGCGTGTCTGCGCTGCTGCGCCAGAGGCGCGGCTGGGAACCGCA 180  
DB 121 gcccctgcgcgctgctgcgcgctgctgcccagggcgggcgggcgggcgagc 180  
QY 181 TCGCGTGTACTGAAACGCTCAACACGACCTGCGGCGAGAGGCTACACCGTCAGGT 240  
DB 181 tgcggtgtactgaaacagctccacacagcactgcgcgagagggctacacgcgtcaggt 240  
QY 241 GAACGTGAACGACTATCTGGATATTTACTGCCGCACTACAAACGCTCGGGGTGGGCC 300  
DB 241 gaacgtgaacgactatctggatatttactgcccgcactacaacagctcgggggtggccc 300  
QY 301 CGGGCGGGGACCGGGCGCGGAGGCGGCGAGAGCAGTACGTGCTGTACATGGTGAGCGG 360  
DB 301 cggggcgggagccggggcgggagggcgggcgagcagtcgctgctacatggtagcgcg 360  
QY 361 CAACGGCTACCGCAGCTCAACCGCCAGCGGCTTCAAGGCTGGAGTGAACCGGCC 420  
DB 361 caacgctacgcacactgcaacgcagccagggcttcaagcgctggagtgcaacccggcc 420  
QY 421 GCACCCCGGCACAGCCCCATCAAGTTCTCGGAAGTTCAGAGCGCTACAGCGCCCTCTC 480  
DB 421 gcaccccgccacagccccatcaagtcttcggagaagttccagcgctcacagcgctctc 480  
QY 481 TCTGGCTACGAGTCCAGCGCGGCGCAGTACTACTACTATCTCCAGCCCACTCAAA 540  
DB 481 tctggctacgagttccacgcggcgagtgactactactactactccacgcccactcaaa 540  
QY 541 CCGTCACTGGAAGTCTCTGAGGATGAAGGTGTCGCTGCTGCGGCTCCACATCGCACTC 600  
DB 541 cctgcaactggaggtctctgagagatgaaggttctgctgctgctgctgctccacatcgactc 600

QY 601 CGGGAGAGAGCCGGTCCCACTCTCCCACTCTCCCACTGACCTGAGCCCAATGTGAAGATCAA 660  
DB 601 cggggagagcgggtcccccactctcccactctcccactggtcccaatgtgaagatcaa 660  
QY 661 CGTCTGGAAGACTTTGAGGGAGAGAACCTCAGCTGCCCCAAGCTTGAGAAGAGCATCAG 720  
DB 661 cgtgctggaagactttgagggagagaaacctcagtgccccagcttgagaagagcatcag 720  
QY 721 CGGGACCAAGCCCAACCGGAACACCTGCCCCCTGGCCCTGGGCATCGGCTTCTTCTCAT 780  
DB 721 cgggacacagccccaaacgggaacacctgccccctggcctgggcatcgcttcttctcat 780  
QY 781 GACGTTCTTGGCCTCCTAGCTGTGCCCTTCCCTTCCCTGGGGGGGAGAGATGGGGGCT 840  
DB 781 gacgttcttggcctcctagctgtgccccctccccctgggggggagagatggggcgggct 840  
QY 841 TGGAGGAGGAGGAGGAGCTTGGCCTCTCCAGGAGGAGCTAGTGGGCTAGACCCCTCC 900  
DB 841 tggaaaggagcaggagccttggcctctccaaagggaagcctagtgggctagaccctcc 900  
QY 901 TCCCATGGCTAGAGTGGGGCTGCGACCATACATCTGTGTCGCGCCCTCTACCCCTTCC 960  
DB 901 tcccatgctagaagtggggcctgcaccatacatctgtgcgccccctctacccttcc 960  
QY 961 CCCCACGTAGGCACTGTAGTGGACCAAGCAGCGGGGAGCCATGGGTCCCGAGCAGGTC 1020  
DB 961 cccacgtagggcactgtagtggaccaagcaggggacagcctatgggtcccgagcaggtc 1020  
QY 1021 GTCTCTTCCCAAGATCC 1037  
DB 1021 gtctcttcccaagatcc 1037

RESULT 2  
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ID AA03883 standard; DNA; 1070 BP.  
XX  
AC AA03883;  
XX  
DT 16-MAY-1996 (first entry)  
XX  
DE Eph transmembrane tyrosine kinase family ligand, Efl-2 encoding DNA.  
XX Efl-2; EH1-L; Eph transmembrane tyrosine kinase family ligand;  
KW neurological disorder; identification; diagnosis; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 46..750  
FT /\*tag= a  
FT /product= Efl-2  
XX  
PN WO9527060-A2.  
XX  
PD 12-OCT-1995.  
XX  
PF 04-APR-1995; 95WO-US04208.  
XX  
PR 21-OCT-1994; 94US-0327423.  
PR 04-APR-1994; 94US-0222075.  
PR 12-APR-1994; 94US-0229402.  
PR 01-SEP-1994; 94US-0299567.  
XX  
PA (REGG-) REGENERON PHARM INC.  
XX Aldrich TH, Davis S, Gale N, Goldfarb M, Maisonnier PC;  
PI Yancopoulos GD;  
XX  
DR WPI; 1995-358635/46.  
DR P-PSDB; AAR82605.  
XX  
PT Ligands which bind Eph family receptors - used in the diagnosis of





















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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 20:18:44 ; Search time 65.52 seconds  
(without alignments)  
3887.698 Million cell updates/sec

Title: US-09-904-954-1

Perfect score: 1037

Sequence: 1 GGATCTTGAACGAGACGAC.....GTCTGTCGTTCCAGATCC 1037

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1037	100.0	1037	1	US-08-240-124-1
2	1037	100.0	1037	1	US-08-453-943-1
3	1037	100.0	1037	2	US-09-057-121-1
4	1037	100.0	1037	4	US-09-358-734-1
5	907.4	87.5	1070	1	US-08-299-567-8
6	151.8	14.6	642	1	US-09-609-324A-9
7	151.8	14.6	642	2	US-08-920-440B-9
8	151.8	14.6	642	4	US-09-173-492-9
9	151.8	14.6	642	4	US-09-173-133-9
10	149.2	14.4	783	1	US-08-455-001-3
11	149.2	14.4	783	5	PCT-US95-11869-3
12	149.2	14.4	1809	1	US-08-455-001-1
13	149.2	14.4	1809	5	PCT-US95-11869-1
14	148	14.3	1615	4	US-08-308-814-1
15	135.4	13.1	314	4	US-09-609-324A-7
16	135.4	13.1	314	2	US-08-920-440B-7
17	135.4	13.1	314	4	US-09-173-492-7
18	135.4	13.1	314	4	US-09-173-133-7
19	135.4	13.1	314	4	US-09-165-533-7
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21	128.8	12.4	555	2	US-08-920-440B-1
22	128.8	12.4	555	4	US-09-173-492-1
23	128.8	12.4	555	4	US-09-173-133-1
24	128.8	12.4	555	4	US-09-165-533-1
25	128.8	12.4	555	5	PCT-US95-12779-1
26	128.8	12.4	555	5	PCT-US95-15781-1
27	116.4	11.2	1480	1	US-08-448-736-11

28 116.4 11.2 1480 1 US-08-452-779-11 Sequence 11, Appl  
29 116.4 11.2 1480 1 US-08-445-065-11 Sequence 11, Appl  
30 116.4 11.2 1480 3 US-08-959-524-11 Sequence 11, Appl  
31 116.4 11.2 1498 1 US-08-321-162-1 Sequence 1, Appl  
32 116.4 11.2 1498 1 US-08-441-216-1 Sequence 1, Appl  
33 104 10.0 1728 3 US-08-379-802-1 Sequence 1, Appl  
34 104 10.0 1728 3 US-09-048-129-1 Sequence 1, Appl  
35 104 10.0 1728 4 US-09-048-079-1 Sequence 1, Appl  
36 104 10.0 1839 1 US-08-442-248-3 Sequence 3, Appl  
37 104 10.0 1839 1 US-08-440-815-3 Sequence 3, Appl  
38 104 10.0 1839 4 US-08-486-449-3 Sequence 3, Appl  
39 103.4 10.0 636 1 US-08-240-124-3 Sequence 3, Appl  
40 103.4 10.0 636 1 US-08-453-943-3 Sequence 3, Appl  
41 103.4 10.0 636 2 US-09-057-121-3 Sequence 3, Appl  
42 103.4 10.0 636 4 US-09-358-734-3 Sequence 3, Appl  
43 102 9.8 687 5 PCT-US95-15781-4 Sequence 4, Appl  
44 55.2 5.3 10348 2 US-08-457-273B-41 Sequence 41, Appl  
45 55.2 5.3 10348 3 US-08-556-419-13 Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-08-240-124-1  
; Sequence 1, Application US/08240124  
; Patent No. 5516658  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240,124  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1037 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA

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; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: hek-L A2  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 83...799  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 83...139  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 140...796  
US-08-240-124-1

Query Match 100.0%; Score 1037; DB 1; Length 1037;  
Best Local Similarity 100.0%; Pred. No. 1.8e-194;  
Matches 1037; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATCTTGGACGAGCAGCCTGCTGGAGAACCGGGAGCGCGGGCTCAGTCGGGGGCG 60  
DB 1 GGATCTTGGACGAGCAGCCTGCTGGAGAACCGGGAGCGCGGGCTCAGTCGGGGGCG 60  
QY 61 GCGCGGCGGGGCTCCGGGATGCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 61 GCGCGGCGGGGCTCCGGGATGCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
QY 121 GCGCGTGGCGTGTGCGCGCTGCTGGCCCAAGGGCCGAGGGGCGCTGGGAAACCGCA 180  
DB 121 GCGCGTGGCGTGTGCGCGCTGCTGGCCCAAGGGCCGAGGGGCGCTGGGAAACCGCA 180  
QY 181 TCGCGTGACTGGAAACAGCTCAACACAGCAGCTGCGCGGAGAGGGCTACACCGTCAGGT 240  
DB 181 TCGCGTGACTGGAAACAGCTCAACACAGCAGCTGCGCGGAGAGGGCTACACCGTCAGGT 240  
QY 241 GAACCTGAACGACTATCTGGATATTACTGCGCGCACTACACAGCTCGGGGTGGGCCC 300  
DB 241 GAACCTGAACGACTATCTGGATATTACTGCGCGCACTACACAGCTCGGGGTGGGCCC 300  
QY 301 CGGGCGGGACCGGGCCCGGAGGCGGAGAGCAGTACGTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 301 CGGGCGGGACCGGGCCCGGAGGCGGAGAGCAGTACGTGCTGCTGCTGCTGCTGCTGCTGCT 360  
QY 361 CNAAGGCTACCGCAGCTGCAAGCGCAGCGAGGGCTTCAAGCGCTGGAGTGAACCGGCC 420  
DB 361 CNAAGGCTACCGCAGCTGCAAGCGCAGCGAGGGCTTCAAGCGCTGGAGTGAACCGGCC 420  
QY 421 GCACGCCCGCACAGCCCATCAAGTTCTCGGAGAGTTCCAGCGCTACAGCGCTTCTC 480  
DB 421 GCACGCCCGCACAGCCCATCAAGTTCTCGGAGAGTTCCAGCGCTACAGCGCTTCTC 480  
QY 481 TCTGGGCTACGAGTTCACGCGGCGCAGAGTACTACTACTACTACTACTACTACTACTACT 540  
DB 481 TCTGGGCTACGAGTTCACGCGGCGCAGAGTACTACTACTACTACTACTACTACTACTACT 540  
QY 541 CCGTCACTGGAAGTCTGAGGATGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 541 CCGTCACTGGAAGTCTGAGGATGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 601 CGGGGAGAGCGGTCCTCCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 660  
DB 601 CGGGGAGAGCGGTCCTCCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 660  
QY 661 CGTGTGGAAGCTTTGAGGAGAGAACCCCTCAGGTGCGGCTGAGAGAGCATCAG 720  
DB 661 CGTGTGGAAGCTTTGAGGAGAGAACCCCTCAGGTGCGGCTGAGAGAGCATCAG 720  
QY 721 CGGGACACCGCCCAACCGGACACCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCT 780  
DB 721 CGGGACACCGCCCAACCGGACACCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCT 780  
QY 781 GACGCTTCTGCGCTCCTAGCTCTGCGCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 840

DB 781 GACGCTTCTGCGCTCCTAGCTCTGCGCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 840  
QY 841 TGGAGGAGCAGGAGCCTTTGGCCTCTCCTCAAGGAAGCCTAGTGGGCTAGACCCCTCC 900  
DB 841 TGGAGGAGCAGGAGCCTTTGGCCTCTCCTCAAGGAAGCCTAGTGGGCTAGACCCCTCC 900  
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QY 961 CCCACGCTAGGCACTGTAGTGGACCAAGCAGCGGGGACAGCCATGGTCCCGAGAGGTC 1020  
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QY 1021 GTCTCGTTCCAAAGATCC 1037  
DB 1021 GTCTCGTTCCAAAGATCC 1037

RESULT 2  
US-08-453-943-1  
; Sequence 1, Application US/08453943  
; Patent No. 5738844  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: GERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/453.943  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/240.124  
; FILING DATE: 09-MAY-1994  
; APPLICATION NUMBER: US 08/161.132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114.426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109.745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1037 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO

ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: hex-L A2  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 83...799  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 83...139  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 140...796  
US-08-453-943-1

Query Match 100.0%; Score 1037; DB 1; Length 1037;  
Best Local Similarity 100.0%; Pred. No. 1.8e-194;  
Matches 1037; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCTTGAACGAGACGACCTGTGGAGAACCGGGAGCGGGGCTCAGTCGGGGGGC 60  
Db 1 GGATCTTGAACGAGACGACCTGTGGAGAACCGGGAGCGGGGCTCAGTCGGGGGGC 60

Qy 61 GCGGCGGCGGCGCTCGGGGATGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCT 120  
Db 61 GCGGCGGCGGCGCTCGGGGATGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCT 120

Qy 121 GCCCGTGGCGTGTGCGGCTGTGGCCCAAGGGCCGAGGGGCGCTGGGAACCGGCA 180  
Db 121 GCCCGTGGCGTGTGCGGCTGTGGCCCAAGGGCCGAGGGGCGCTGGGAACCGGCA 180

Qy 181 TCGCGTGTACTGGAACAGCTCCAAACAGACCTGCGGCGAGAGGCTACACCGTSCAGGT 240  
Db 181 TCGCGTGTACTGGAACAGCTCCAAACAGACCTGCGGCGAGAGGCTACACCGTSCAGGT 240

Qy 241 GAACGTGAACGACTATCTGGATATTTACTGCGGCGCTACACAGCTCGGGGGTGGGCC 300  
Db 241 GAACGTGAACGACTATCTGGATATTTACTGCGGCGCTACACAGCTCGGGGGTGGGCC 300

Qy 301 CGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
Db 301 CGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360

Qy 361 CAACGGCTACCGGCTGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
Db 361 CAACGGCTACCGGCTGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420

Qy 421 GCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480  
Db 421 GCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480

Qy 481 TCTGGGCTACGAGTTTCCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
Db 481 TCTGGGCTACGAGTTTCCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540

Qy 541 CCGTCACTGGAAGTGTCTGAGATGAAGTGTCTGCTGCGGCGGCGGCGGCGGCGGCGG 600  
Db 541 CCGTCACTGGAAGTGTCTGAGATGAAGTGTCTGCTGCGGCGGCGGCGGCGGCGGCGG 600

Qy 601 CGGGGAGAGCGGCTCCCACTCTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCC 660  
Db 601 CGGGGAGAGCGGCTCCCACTCTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCC 660

Qy 661 CCGTCACTGGAAGTGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
Db 661 CCGTCACTGGAAGTGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

Qy 721 CGGGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780  
Db 721 CGGGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780

Qy 781 GACGTCTTGGCGCTTCTAGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840  
Db 781 GACGTCTTGGCGCTTCTAGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840

Db 781 GACGTCTTGGCGCTTCTAGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 840

Qy 841 TGAAG 900

Db 841 TGAAG 900

Qy 901 TCCCATGGCTAGAAAGTGGGGCTGCACCATATCATCTGTGTGCGGCGGCGGCGGCGGCT 960

Db 901 TCCCATGGCTAGAAAGTGGGGCTGCACCATATCATCTGTGTGCGGCGGCGGCGGCGGCT 960

Qy 961 CCCACGTAGGCGCTGTAGTGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020

Db 961 CCCACGTAGGCGCTGTAGTGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020

Qy 1021 GTCTCGTTCCCAAGATCC 1037

Db 1021 GTCTCGTTCCCAAGATCC 1037

RESULT 3  
US-09-057-121-1  
; Sequence 1, Application US/09057121  
; Patent No. 5969110  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,121  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/240,124  
; FILING DATE:  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1037 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

IMMEDIATE SOURCE:  
CLONE: hek-L A2  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 83...799  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 83...139  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 140...796  
US-09-057-121-1

Query Match 100.0%; Score 1037; DB 2; Length 1037;  
Best Local Similarity 100.0%; Pred. No. 1.8e-194;  
Matches 1037; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATCTTGAACGAGACGACCTGCTGGAGAACCGGGAGCGGGGCTCAGTCGGGGGC 60  
Db 1 GGATCTTGAACGAGACGACCTGCTGGAGAACCGGGAGCGGGGCTCAGTCGGGGGC 60  
QY 61 GCGGGGGGGGGCTCCGGGGATGCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCT 120  
Db 61 GCGGGGGGGGGCTCCGGGGATGCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCT 120  
QY 121 GCCCGTGGCGCTGCTGCCGCTGCTGCCCAAGGGCCGGAGGGGGCTGGAAACCGGCA 180  
Db 121 GCCCGTGGCGCTGCTGCCGCTGCTGCCCAAGGGCCGGAGGGGGCTGGAAACCGGCA 180  
QY 181 TCGGGTGTACTGGACAGCTCAACGAGCAGCTGGGGGAGAGGGGTACACCGTGCAGGT 240  
Db 181 TCGGGTGTACTGGACAGCTCAACGAGCAGCTGGGGGAGAGGGGTACACCGTGCAGGT 240  
QY 241 GAACGTGAACGACTATCTGGATATTACTGCCGCACTACAACAGCTCGGGGTGGGCC 300  
Db 241 GAACGTGAACGACTATCTGGATATTACTGCCGCACTACAACAGCTCGGGGTGGGCC 300  
QY 301 CGGGGGGAGCGGGGGCGGGAGCGGGGAGGAGTACGTGCTGTACATGTGAGCGG 360  
Db 301 CGGGGGGAGCGGGGGCGGGAGGCGGGGAGGAGTACGTGCTGTACATGTGAGCGG 360  
QY 361 CAACGGCTACCGCACCTGCAACGCGCAGCGAGGCTTCAAGCGCTGGGAGTGAACGGCC 420  
Db 361 CAACGGCTACCGCACCTGCAACGCGCAGCGAGGCTTCAAGCGCTGGGAGTGAACGGCC 420  
QY 421 GCACGCCCCGACAGCCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCTTCTC 480  
Db 421 GCACGCCCCGACAGCCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCTTCTC 480  
QY 481 TCTGGGTACGAGTTCCAGCGGGCCAGAGTACTACTACATCTCCACGCCCACTCACAA 540  
Db 481 TCTGGGTACGAGTTCCAGCGGGCCAGAGTACTACTACATCTCCACGCCCACTCACAA 540  
QY 541 CCGTGCAGTGAAGTCTCTGAGGATGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 541 CCGTGCAGTGAAGTCTCTGAGGATGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 601 CGGGGAGAGCGCGTCCCACTCTCCCCCAGTTCCACATGGGCCCCCAATGTGAAGATCAA 660  
Db 601 CGGGGAGAGCGCGTCCCACTCTCCCCCAGTTCCACATGGGCCCCCAATGTGAAGATCAA 660  
QY 661 CTGCTGGAAGACTTTGAGGAGAGAACCCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720  
Db 661 CTGCTGGAAGACTTTGAGGAGAGAACCCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720  
QY 721 CGGGACACGCCCCAAACGGGAACCTGCCCTGCGCTGGGCATCGCCTTCTCTCAT 780  
Db 721 CGGGACACGCCCCAAACGGGAACCTGCCCTGCGCTGGGCATCGCCTTCTCTCAT 780  
QY 781 GACGTTCTTGGCTCCTAGCTCTGCCCTCCCTCGGGGGGAGAGATGGGGCGGGCT 840  
Db 781 GACGTTCTTGGCTCCTAGCTCTGCCCTCCCTCGGGGGGAGAGATGGGGCGGGCT 840

QY 841 TGAAGGAGCAGGAGCCCTTTGGCCTCTCAAGGGAAGCCTAGTGGCCCTAGACCCCTCC 900  
Db 841 TGAAGGAGCAGGAGCCCTTTGGCCTCTCAAGGGAAGCCTAGTGGCCCTAGACCCCTCC 900  
QY 901 TCCCATGGCTAGAAAGTGGGGCTGCACCATACATCTGTCTCGGCCCTCTACCCCTTCC 960  
Db 901 TCCCATGGCTAGAAAGTGGGGCTGCACCATACATCTGTCTCGGCCCTCTACCCCTTCC 960  
QY 961 CCCACGTTAGGCACTGTAGTGGACCAACGACGCGGACAGCATGGTCCCGACAGGTC 1020  
Db 961 CCCACGTTAGGCACTGTAGTGGACCAACGACGCGGACAGCATGGTCCCGACAGGTC 1020  
QY 1021 GTCTGTTCCAAAGATCC 1037  
Db 1021 GTCTGTTCCAAAGATCC 1037  
RESULT 4  
US-09-358-734-1  
; Sequence 1, Application US/09358734  
; Patent No. 6274117  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/358,734  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/240,124  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1037 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: hek-L A2  
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: 83..799
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 83..139
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 140..796
US-09-358-734-1

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Query Match      100.0%; Score 1037; DB 4; Length 1037;
Best Local Similarity 100.0%; Pred. No. 1.8e-194;
Matches 1037; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	GGATCTTTGGAAACGAGACGAC <sup>Δ</sup> CTGCTGGAGAAGCCGGAGACGGGGGCTCAGTCGGGGGCG	60
Db	1	GGATCTTTGGAAACGAGACGACCTGCTGGAGAAGCCGGAGACGGGGGCTCAGTCGGGGGCG	60
Qy	61	GGCGGGCGGCGGCTCCGGGGATGGCGGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	120
Db	61	GGCGGGCGGCGGCTCCGGGGATGGCGGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	120
Qy	121	GCCCGTCCGCTGCTGCGCTGCTGCGCCCAAGGCCCCGAGGGGCGCTGGGAACACCGCA	180
Db	121	GCCCGTCCGCTGCTGCGCTGCTGCCCCAAGGCCCCGAGGGGCGCTGGGAACACCGCA	180
Qy	181	TGCGGTCTACTGGAACAGCTTCCAAACAGCACTTACGCCGCACTACACAGCTCGGGGTGGGCC	240
Db	181	TGCGGTCTACTGGAACAGCTTCCAAACAGCACTTCGCGCAGAGGGGTACACGCTGCAGT	240
Qy	241	GAAGCTCAACGACTATCTGGATATTACTGCCCGCACTACACAGCTCGGGGTGGGCC	300
Db	241	GAAGCTCAACGACTATCTGGATATTACTGCCCGCACTACACAGCTCGGGGTGGGCC	300
Qy	301	CGGGCGGGACCGGGGCCCGGAGCGCGGGCAGACAGTACGTGCTGTACATGCTGAGCGC	360
Db	301	CGGGCGGGACCGGGGCCCGGAGCGGGCAGACAGTACGTGCTGTACATGCTGAGCGC	360
Qy	361	CAACGGCTACCGCACTGCAACGCCAGCCAGCGGCTTCACGCGTGGAGTGCACCGGCC	420
Db	361	CAACGGCTACCGCACTGCAACGCCAGCCAGCGGCTTCACGCGTGGAGTGCACCGGCC	420
Qy	421	GCAGCCCGGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCTTCTC	480
Db	421	GCAGCCCGGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCTTCTC	480
Qy	481	TCTGGGTACGAGTTCCACGCCGGCCACAGTACTACTACATCTCACGCCCACTCACAA	540
Db	481	TCTGGGTACGAGTTCCACGCCGGCCACAGTACTACTACATCTCACGCCCACTCACAA	540
Qy	541	CCTGCATGGAAGTGCTGAGGATGAAGTGTTCTGCTGCTGGCCCTCCACATCGCACTC	600
Db	541	CCTGCATGGAAGTGCTGAGGATGAAGTGTTCTGCTGCTGGCCCTCCACATCGCACTC	600
Qy	601	CGGGGAAGCCGCTCCCACTCTCCCCAGTTTCACCATGGGGCCCCAATGTGAAGATCAA	660
Db	601	CGGGGAAGCCGCTCCCACTCTCCCCAGTTTCACCATGGGGCCCCAATGTGAAGATCAA	660
Qy	661	CGTGCTGGAAGACTTTGAGGGAGAACCCCTCAGTGTCGCCAAGCTTTGAGAAGAGCATAG	720
Db	661	CGTGCTGGAAGACTTTGAGGGAGAACCCCTCAGTGTCGCCAAGCTTTGAGAAGAGCATAG	720
Qy	721	CGGACACAGCCCCAAGCGGAACACCTGCCCCCTTGGCGGTGGGGATCGCCTTCTTCTCAT	780
Db	721	CGGACACAGCCCCAAGCGGAACACCTGCCCCCTTGGCGGTGGGGATCGCCTTCTTCTCAT	780
Qy	781	GACGTTCTTGGCTTCCTAGCTCTGCCCTTCCCTCGGGGGGAGAGATGGGGCGGGCT	840
Db	781	GACGTTCTTGGCTTCCTAGCTCTGCCCTTCCCTCGGGGGGAGAGATGGGGCGGGCT	840
Qy	841	TGGAAGGACGAGGAGCCTTTTGGCCTCTCCAAAGGAAGCCTAGTGGGCTTAGACCCCTCC	900

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Db 841 TGAAGAGCAGGAGGCGCTTTGGCCCTCTCCAAAGGAAGCCTAGTGGGCTAGACCCCTCC 900
Qy 901 TCCCATGGCTAGAAAGTGGGSCCTGCACCATACATCTGTGCGCCCCCTCTACCCCTTCC 960
Db 901 TCCCATGGCTAGAAAGTGGGSCCTGCACCATACATCTGTGCGCCCCCTCTACCCCTTCC 960
Qy 961 CCCACGCTAGGGCACTGTAGTGGACCAACAGCAGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
Db 961 CCCACGCTAGGGCACTGTAGTGGACCAACAGCAGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
Qy 1021 GTCTCGTTCCCAAGATCC 1037
Db 1021 GTCTCGTTCCCAAGATCC 1037

RESULT 5
US-08-299-567-8
; Sequence 8, Application US/08299567
; Patent No. 5747033
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
; TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,567
; FILING DATE: 01-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler, Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-299-567-8

```

	Query Match	87.5%	Score	907.4;	DB 1;	Length	1070;			
	Best Local Similarity	96.3%;	Pred. No.	3.6e-169;						
	Matches	939;	Conservative	0;	Mismatches	24;	Indels	12;	Gaps	1;
Qy	44	GGGCTCACTCGGGGGCGGCGCGCGCTCCGGGGATGGCGCGCTCCGCTGC	GTG	103						
Db	7	GAGATCCATTGTGCTGGAAAGCGCGCGCGCTCCGGGGATGGCGCGCTCCGCTGC	GTG	66						
Qy	104	CTGCTGCTGCTGCTCGTGCCTCGTGCCTGTGTCGCCGTCTGGCCCAAGGGCCCGAGGG	163							
Db	67	CTGCTGCTGCTGCTGTCGCCGTGCTGTCGCCGTCTGGCCCAAGGGCCCGAGGG	126							
Qy	164	GGCTGGGAACCGGCATCGGTGTACTGGAAACAGCTCAACCCAGCACCTTGGGGCGAGAG	223							
Db	127	GGCTGGGAACCGGCATCGGTGTACTGGAAACAGCTCAACCCAGCACCTTGGGGCGAGAG	186							











Db 445 CACCCTCTCTTTGGGCTTCGAGTTCCGTCGCCGCCACGAGTATTACTACATCTCTGC 504  
QY 529 GCCACTCAACACCTG 544  
Db 505 GTCTCCCGGAACGTG 520

## RESULT 12

US-08-455-001-1  
; Sequence 1, Application US/08455001  
; Patent No. 5795734  
; GENERAL INFORMATION:  
; APPLICANT: Flanagan, John G.  
; APPLICANT: Cheng, Hwai-Jong  
; TITLE OF INVENTION: Eph Receptor Ligands, and Uses Related  
; TITLE OF INVENTION: Therto  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,001  
; FILING DATE: 31 MAY 1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: HMI-011CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1809 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 265..891  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..264  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: 892..1809  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 255..324  
US-08-455-001-1

Query Match 14.4%; Score 149.2; DB 1; Length 1809;  
Best Local Similarity 62.6%; Pred. No. 4.5e-21;  
Matches 322; Conservative 0; Mismatches 148; Indels 44; Gaps 4;

QY 53 CGGGGGCGGGCGGGCGGCTCGGG--ATGCGGGCGGCTCGGCTGCTGCTGCTGC 110  
Db 233 CAGAGGACGAGCGCGCGACACGCGGCGCATGGCCGCGCAGCGCGCGCTGCTGC 292  
QY 111 TGCTCTCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 170  
Db 293 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352

QY 171 GAAACCGGATCGGGTGTACTGGAACAGCTCCAACACAGACACCTGCGGC----- 218  
Db 353 CTGACCGATACGACGCTACTTGAACCGTAGCAACCCAGGTTTCAGGTGAGCGTGTGG 412  
QY 219 -----GAGAGGGCTACACCGTGCAGGTGAAGCTGAACGACTATCTGGATATTTACTGCC 272  
Db 413 GTGATGGGGCGGCTATACCGTGGAGGTGAGCATCAACGACTACCTGGATATCTACTGCC 472  
QY 273 CGCACTACAACAGCTCGGGGTGGGCCCGGGCGGGACCGGGCGGCGGAGCGGGGCGAG 332  
Db 473 CACACTA-----CGGGCGCGCGTGCCTCCCGGCTGAGCGCATGG 511  
QY 333 AGCACTAGTGTGTACATGTGAGCGGACGCGACGCTACCGCACTGCAACGCCAGCCAG- 391  
Db 512 AGCGGTACATCTGTACATGTGTAATGTTGAGGGCCACGCCCTCTGTACCACCGCAGC 571  
QY 392 --GGCTTCAAGCGCTGGAGTGCACCGCGCGACGCCCGCGCACAGCCCCCATCAAGTTCT 449  
Db 572 GAGGCTTCAAGCGCTGGGAATGCAACCGCGCGCGGCGGCGGAGCCCTCAAGTTCT 631  
QY 450 CGGAGAAGTTCACGCGCTACAGCGCTTCTCTCTGGGGTACGAGTTCCACGCCGCGCAGG 509  
Db 632 CAGAGAAGTTCACACTCTTCAACCCCTTTTCCCTGGGCTTTGAGTTCCGGCCTGCGCAGG 691  
QY 510 AGTACTACTACATCTCCAGCGCCACTCACAACCT 543  
Db 692 AATACTACTACATCTCTGCCACACACTCCCAACCT 725

## RESULT 13

PCT-US95-11869-1  
; Sequence 1, Application PC/TUS9511869  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Eph Receptor Ligands, and Uses Related  
; TITLE OF INVENTION: Therto  
; NUMBER OF SEQUENCES: 5  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/11869  
; FILING DATE: 19-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: HMI-011CPPC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1809 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 265..891  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..264  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: 892..1809  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 255..324  
PCT-US95-11869-1

[illegible][illegible]



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OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 21:26:30 ; Search time 3673.16 Seconds  
(without alignments)  
6107.926 Million cell updates/sec

Title: US-09-904-954-1

Perfect score: 1037

Sequence: 1 GATCTTGACAGACGAC.....GTGCTCTCGTCCAGATCC 1037

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1037	100.0	1037	34	US-09-904-954-1
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4	1033.8	99.7	1037	5	US-08-161-132-1
5	988.8	95.4	1761	56	US-60-172-373-10727
6	988.8	95.4	1761	66	US-60-278-258-13410
7	987	95.2	1743	18	US-09-440-302A-838
8	917.8	88.5	1743	29	US-09-733-756-1
9	907.4	87.5	1070	6	US-08-229-402-8
10	907.4	87.5	1070	7	US-08-327-423-8
11	773	74.5	818	27	US-09-698-010-11586
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14	411.8	39.7	421	16	US-09-287-618-6642
15	392	37.8	392	16	US-09-221-481-182
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31	308.8	29.8	339	20	US-09-534-853-8616

32	304.2	29.3	600	18	US-09-404-549-2399	Sequence 2399, Appl
33	304.2	29.3	600	18	US-09-404-549A-2399	Sequence 2399, Appl
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35	292.2	28.2	575	18	US-09-474-434-715	Sequence 715, Appl
36	292.2	28.2	575	56	US-60-173-686-253	Sequence 253, Appl
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39	282.2	27.2	390	27	US-09-698-010-7881	Sequence 7881, Appl
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41	231.2	24.2	276	20	US-09-534-653-8650	Sequence 8650, Appl
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44	239.4	23.1	258	23	US-09-605-778A-440	Sequence 440, Appl
45	234.6	22.6	279	6	US-08-222-075-5	Sequence 5, Appl

## ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: CERRETI, DOUGLAS P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09282
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,132
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/114,426
; FILING DATE: 30-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/109,745
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SEESE, KATHRYN A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2814-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
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; FEATURE:

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; Sequence 1, Application US/09904954  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; CERRETI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
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; FILING DATE: 30-AUG-1993  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SESE, KATHIRN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1037 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
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; LOCATION: 140..796  
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3	987	95.2	987	5	US-09-440-302B-838	Sequence 838, App
4	392	37.8	392	5	US-09-442-366A-292	Sequence 292, App
5	391	37.7	391	5	US-09-440-302B-241	Sequence 241, App
6	350.8	33.8	442	5	US-09-918-995-27387	Sequence 27387, A
7	153.8	14.8	1594	5	US-09-053-375B-1095	Sequence 1095, Ap
8	117	11.3	1557	5	US-09-919-039-161	Sequence 161, App
9	116.4	11.2	1480	1	PCR-US02-13644-14	Sequence 14, Appl
10	116.4	11.2	1480	5	US-09-053-375B-1504	Sequence 1504, Ap
11	116.4	11.2	1480	5	US-09-442-384B-743	Sequence 743, App
12	116.4	11.2	1480	5	US-09-440-302B-837	Sequence 837, App
13	116.4	11.2	1480	7	US-10-007-926A-227	Sequence 227, App
14	116.4	11.2	1480	7	US-10-136-819-14	Sequence 14, Appl
15	116.4	11.2	1480	7	US-10-171-311-49	Sequence 49, Appl
16	116.4	11.2	1480	7	US-10-171-581-190	Sequence 190, App
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20	116.4	11.2	1496	6	US-10-210-951-39	Sequence 39, Appl
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23	116.4	11.2	1496	6	US-10-230-417-287	Sequence 287, App
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Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 420  
QY 446 TTCTCGGAGAAAGTTCACAGCTTACAGCGCTTCTCTCTGCGGTACGAGTTCACCGCGC 505  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 480  
QY 506 CACGAGTACTACTACATCTCCAGCGCCCACTACAACTTGCATGGAAGTGTGAGGATG 565  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 540  
QY 566 AAGGTGTTCTGCTGTGCGCTTCCACATCGCACTCCGGGGAGAACCGCTCCCACTCTC 625  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 600  
QY 626 CCCCAGTTACCATGGGCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 660  
QY 686 AACCTCAGGTGCCCAAGCTTGAGAGAGCATCAGCGGACCGACCGCCCAACGGGAACAC 745  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 720  
QY 746 CTGCCCTGGCGGTGGGATCGCTTCTCTCATGAGCTTCTGGCCTCTCTAGCTCTGC 805  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 780  
QY 806 CCCCCTCCCTGGGGGGAGAGATGGGGGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 865  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 840  
QY 866 TCTCCAGGGAAGCCTAGTGGGCTTAGACCCCTCTCTCCATGGGTAGAGTGGGCTTC 925  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 900  
QY 926 ACCATACATCTGTGTCGCCCGCCCTCTACCCCTTCCCGCCACGTAGGACACTGTAGTGAC 985  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 960  
QY 986 CAAGCACGGGACAGCCATGGTCCCG 1012  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 987

RESULT 2  
US-09-053-375B-186  
; Sequence 186, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; FILE REFERENCE: CLON-006  
; CURRENT APPLICATION NUMBER: US/09/053,375B  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 186  
; LENGTH: 987  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-053-375B-186

Query Match 95.28; Score 987; DB 5; Length 987;

Best Local Similarity 100.0%; Pred. No. 1.6e-154;  
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0:  
QY 26 GGAGAAAGCCGGAGCGCGGCTAGTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 85  
Db 1 ggagaaagccggagcgcggggtcagtcgggggggggggggggggggggggggggggg 60  
QY 86 CGGGCGGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 145  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 120  
QY 146 GCCCAGGGCCCGGAGGGGCGCTGGGAACCGGCATGCGGTGTACTGGAAACAGCTTCAAC 205  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 180  
QY 206 CAGCACTTCCGGGAGAGGGCTACACCGTGCAGGTGAACGTGAACGATATCTGTGATATT 265  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 240  
QY 266 TACTGCCCGCACTACAAAGCTCGGGGTGGGGTGGGGGGGGGGGGGGGGGGGGGGGG 325  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 300  
QY 326 GGGGAGAGAGCTAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 385  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 360  
QY 386 AGCCAGGGCTTCAAGCGCTGGAGTGCACCGCGCGCACCGCCCGCACAGCCCGCATCAAG 445  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 420  
QY 446 TTCTCGGAGAAAGTTCACAGCTTACAGCGCTTCTCTCTGCGGTACGAGTTCACCGCGC 505  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 480  
QY 506 CACGAGTACTACTACATCTCCAGCGCCCACTACAACTTGCATGGAAGTGTGAGGATG 565  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 540  
QY 566 AAGGTGTTCTGCTGTGCGCTTCCACATCGCACTCCGGGGAGAACCGCTCCCACTCTC 625  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 600  
QY 626 CCCCAGTTACCATGGGCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 660  
QY 686 AACCTCAGGTGCCCAAGCTTGAGAGAGCATCAGCGGACCGACCGCCCAACGGGAACAC 745  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 720  
QY 746 CTGCCCTGGCGGTGGGATCGCTTCTCTCATGAGCTTCTGGCCTCTCTAGCTCTGC 805  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 780  
QY 806 CCCCCTCCCTGGGGGGAGAGATGGGGGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 865  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 840  
QY 866 TCTCCAGGGAAGCCTAGTGGGCTTAGACCCCTCTCTCCATGGGTAGAGTGGGCTTC 925  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 900  
QY 926 ACCATACATCTGTGTCGCCCGCCCTCTACCCCTTCCCGCCACGTAGGACACTGTAGTGAC 985  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 960  
QY 986 CAAGCACGGGACAGCCATGGTCCCG 1012  
Db |||||||cgcactacaaagctcgggggtggccccggggcgagccgggccccggagcc 987

RESULT 3

```
US-09-440-302B-838
; Sequence 838, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP1
; CURRENT APPLICATION NUMBER: US/09/440,302B
; PRIOR FILING DATE: 1999-11-17
; CURRENT FILING DATE: 1999-11-17
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 838
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-440-302B-838

Query Match      95.2%; Score 987; DB 5; Length 987;
Best Local Similarity 100.0%; Pred. No. 1.6e-154;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 GGAGAACCGGGAGCGGGGCTCAGTCGGGGGGCGCGCGGGGCTCCGGGGATG 85
Db 1 ggagaagcgggagcgggctcagtcggggggcgcgcgcgcgcgcggggatg 60
QY 86 GCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 145
Db 61 gcggcgctccgctgctgctgctgctgctgctgctgctgctgctgctgctg 120
QY 146 GCCAAGCGCGGGAGGGGCTGGGAAACCGGCATCGGTGTACTGGAACAGCTCCAAC 205
Db 121 gccaaagggcgagggcgctgggaaccgcatcggtgtactggaacagctcaac 180
QY 206 CAGCACTCGCGGGAGAGGGGTACACCGTCGAGTGAACGTGAACGACTATCTGGAT 265
Db 181 cagcactcgcgagaggggtacacgctgaggtgaggtgaggtgaggtgaggtg 240
QY 266 TACTGCCCGCAGTACACAGCTCGGGGTGGGCGCGGGGCGGGGCGGGGCGGAGGC 325
Db 241 tactgcccgacacacagctcggggtggcgccggcgggcgagggcgagggcg 300
QY 326 GGGCAGAGAGTACGTGCTGTACATGGTGAGCGCGCAACGCTACCGCAGCTGCAAGCC 385
Db 301 gggcgagagcagctgctgctgctgctgctgctgctgctgctgctgctgctg 360
QY 386 AGCCAGGGCTTCAAGCGCTGGAGTGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 445
Db 361 agccagggcttcaagcgtggagtgcaacggcgcgcgcgcgcgcgcgcgcgcg 420
QY 446 TTCTCGAGAGTTCACGCGCTACAGCGCTTCTCTCTGGGCTACGAGTTCACGCGCG 505
Db 421 ttcctggagaggttcacagcgtacagcgcttctctgctgctgctgctgctgctg 480
QY 506 CACGAGTACTACTATCTCCACCGCCACTCACACCTGCACTGGAAGTGTCTGAGGATG 565
Db 481 cagagtgactactactctccagcccaactcaacacactgcaactgcaactgca 540
QY 566 AAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 625
Db 541 aaggtgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 600
QY 626 CCCAGTTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 685
Db 601 cccagttcacctagggcgcccaatgtaagatacaactgctggaagactttgagg 660
QY 686 AACCTTCAGGTGCGCAAGTGTGAGAAGAGATCAGCGGGACAGCGCCCAACAGGCAAC 745
Db 661 aacctcaggtgccaagcttgagaagagatcaagcggggacccagcccaaacgg 720
QY 746 CTGCCCTGGCGCGGGCATCGCCTTCTCTCTCATGACGTTCCTTGGCCTCCTAGCTG 805

US-09-442-366A-292
; Sequence 292, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey E.
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-006CIP3
; CURRENT APPLICATION NUMBER: US/09/442,366A
; CURRENT FILING DATE: 1999-11-17
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-292

Query Match      37.8%; Score 392; DB 5; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.3e-56;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 TCCAAACAGCACCTGCGGGGAGAGGGGTACACCGTGCAGGTGAACGACTATCTG 259
Db 1 tccaaacagcacctgcggcgaggggtacacccgtgacagtgacagtgacagctat 60
QY 260 GATATTTACTGCGCGCACTACACAGCTCGGGGTGGGCGCGGGGCGGGGCGGGGCC 319
Db 61 gatatttactgccccgactacacagctcggggtggtggcgggcgggcgggcggg 120
QY 320 GGAGCGGGGCGAGCAGTACGTGCTGTACATGGTGAAGCGCAACGGGTACCGACCTGC 379
Db 121 ggagcgggcgagcagcagtcgtgctgtacatggtgagcgcaacgctacccgct 180
QY 380 AACCGCAGCCAGGGCTTCAACGGCTGGAGTGAACCGCGCGCGCGCGCGCGCGCGCC 439
Db 181 aacgcagcagggcttcaagcgtggagtgcaacggcgcgcgcgcgcgcgcgcg 240
QY 440 ATCAAGTTCGGGAGAAGTTCACGGCTTACAGCGCTTCTCTCTGGGCTACGAGTCCAC 499
Db 241 atcaagttctcggaagagtcagcagcgtctctctctctctctctctctctctct 300
QY 500 GCCGCGCCACGAGTACTACTACTACTCTCCACGCCCTCACAACCTGCAGTGAAGTGTG 559
Db 301 gccgcccacgagtgactactactactctccagcggcggcggcggcggcggcggc 360
QY 560 AGGATGAAGGTGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 591
Db 560 aggatgaaggtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 591
```

Db 361 aggatgaaagatatttcgtctgctgacgcctccac 392

## 5 RESULT

```

US-09-440-302B-241
; Sequence 241, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Lunchev, Alex
; APPLICANT: Chenchik, Alex
; APPLICANT: Kuchashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006GIP11
; CURRENT APPLICATION NUMBER: US/09/440,302B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302B-241

```

Query Match 37.7%; Score 391; DB 5; Length 391;  
Best Local Similarity 100.0%; Pred. No. 4.9e-56;  
Matches 391; Conservative 0; Mismatches 0; Indels

Qy	200	TCCAACGACGACCTGGCGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTG	259
Db	1	tccaacagcacctggcgagagggtacacccgtgcagtgaaactgaacgactatctg	60
Qy	260	GATATTACTGCCGCACTACAACGCTCGGGGTGGCCCGCGGGCGGACCGGGGCC	319
Db	61	gattattacgcgcgcactacaacgctcggggtggcccgggcgagccggggccc	120
Qy	320	GGAGCGGGCGAGAGCAGTAGTACGTGCTGTACATGGTAGCGCGCAACGGCTACCGCACCTGC	379
Db	121	ggaggcgggcgagcagtagcgtgcgtacatggtgagccgaacggctaccgcacctgc	180
Qy	380	AACGCCACCGCAGGGCTTCAAGCGCTGGGAGTGCACCGCGCGACGCCCGCGACAGCGCC	439
Db	181	aacgcgaagcgaggtctcaagcgtggagtgcaacgcggcgacgcgccgcacagcccc	240
Qy	440	ATCAAGTTCTCGAGAGGTTCCAGCGCTACAGCGCCTTCTCTGTGGCTACGAGTTCCAC	499
Db	241	atcaagttcttcggagaagttccagcgctacagcgctctctctggctacaggttccac	300
Qy	500	GCGGCCACGAGTACTACTACTCTCCACGCCCACTCACAACTCGCACTGGGAAGTCTCTG	559
Db	301	gcgcgccacgagtactactacatctccagcccaactcaaacctgcactggaaagtgtctg	360
Qy	560	AGGATGAAGTGTTCTGCTGGCGCTCCA	590
Db	361	agatgaagtgattctctactcgcctcca	391

RESULT

```

RESOLUTION 0
US-09-918-995-27387
; Sequence 27387, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq. Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1993-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: Fastseq for Windows Version 3.0
;

```

; SEQ ID NO 27387  
: LENGTH: 442

```

;
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(442)
; OTHER INFORMATION: n =
US-09-918-995-27387

```

Query Match	33.8%	Score	350.8;	DB	5;	Length	442;
Best Local Similarity	93.8%;	Pred. No.	2.1e-49;				
Matches	364;	Conservative	0;	Mismatches	24;	Indels	0;
						Gaps	0;

Qy	630	AGTTCACCATGGGCCCCAATGTGAAGATCAACCTGCTGGAAGACTTTGAGGGAGAGAACC	689
Db	6	actggaccatccgancctgaggcacaatcgaaangcgtggaagactttgaggagagagaacc	65
Qy	690	CTCAGGTGCCCAACAGCTTGAGAAAGCATCAGCGGGACCAAGCCCAACCGGACACCTGC	749
Db	66	ctcaggtgcacaagcttgattgagcatcagcgsggttcagccccaacagggaacactgc	125
Qy	750	CCCTGGCGCTGGGGCATCGCCCTCTTCCATATACGTTCTTTGGCCTCCTAGCTCTGCCCC	809
Db	126	ccctgycgcgtgggcatacgcccttctccteaagaegttcttggcctcctcagctcgcgcc	185
Qy	810	TCCCTCTGGGGGGGAGAGATGGGGCGGGGTTGGAAAGAGCAGGGAGCCTTTGGCCTCTC	869
Db	186	tccectggggggggagagatggggcggggcttggaaaggagcaggagaccttggcctctc	245
Qy	870	CAAGGGAGCGCTAGTGGCGCTAGACCCCTCCTCCCATGGCTAGAACTGGGGCTGCACCA	929
Db	246	caagggaagcctagtgggcctagacccctcctccatggtctagaagtggggcctgcacca	305
Qy	930	TACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACAGTAGGGCACTGTAGTGGACCAAG	989
Db	306	tacatctgtgcgcgccccctacccttcccccaagtagggcactgtagtgaccaag	365
Qy	990	CACGGGACAGCAATGGGTCCCGAGCAG	1017
Db	366	caagggaacagcctatgggtcccgggcgg	393

## RESULT

```

US-09-053-375B-1095
;
; Sequence 1095, Application US/09053375B
; GENERAL INFORMATION:
;
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1095
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-1095

```

Query Match	14.8%	Score 153.8;	DB 5;	Length 1594;
Best Local Similarity	63.1%	Pred. NO. 6e-17;		
Matches 326:	Conservative	0: Mismatches	147:	Indels 44: Gaps 4:

Qy 50 AGTCGGGGCGGCGGGGGGTCCGGG - ATGGCGGGGTCCGCTGCTGC  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 20 agcagggagcagcgcgcgaggccatggcgccgcgacgcgccgtgc 79  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 108 TGCTGCTGCTGTCCCGTCCCGCTGCTGCCGTGCTGCCAAGGCCCGGAGGGCGC 167

[illegible]



197	QY	AGTCCAACCCAGCACTGCGCGGAGAGGGCTTACACGGTGCAGGTGAACGTGAACGACTAT	256
152	Db	agttcaaatcccaagttccgggaatgagctacacacatacatctgacgtgaatgactact	211
257	QY	CTGGATATTACTGCCCGCACATACAACAGCTCGGGGGTGGCCCGCGGGGCGGACCGGGG	316
212	Db	gtggacatacatctgtccgcacataatgaataactctgtggcagacgtgcgaagt-----	265
317	QY	CCCGGAGGCGGGGAGCAGCAGTACGTGCTTATCTACATGGTGAGCGGCAACGGCTACCGCACCC	376
266	Db	-----gacagtatatactgtacctgtgtgagcatgagagttaccagctgt	310
377	QY	TGCAAGCCGACG---CCAGGGCTTCAAGCGCTGGGAGTGCACACGGCGCGCACGCCCGCGAC	433
311	Db	tgcacgccacagttccaaagaccaaagtccgcgtggcagtgcaacccggcccaagtcccaagcat	370
434	QY	AGCCCATCAAGTTCTCGGAGAGGTTCCAGCGCTACAGCGCTTCTCTCTGGGCTACGAG	493
371	Db	ggccccgagagctgtctgagaagttccacgcttccacacctttcacacctgggcaaggag	430
494	QY	TTCCAGCGCGGCCAGGAGTACTACTACTCTCCAGCGCCCACTCAACACTGCATGGAG	553
431	Db	ttcaagaagcacagctactactacatactccaaacccatccaccagcatgaagacgcg	490
554	QY	TGTCTGAGGATGAAGGTGTTCGTCTGCTGGCGCTCCAC	591
491	Db	tgcttaagtttaagatgactctcagttgcaaaataac	528

```

RESULT 14
US-10-136-819-14
; Sequence 14, Application US/10136819
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Non-viral vesicle vector for cardiac specific gene
; FILE REFERENCE: 6627-Pal198
; CURRENT APPLICATION NUMBER: US/10/136,819
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/287,423
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-136-819-14

```

	Query Match	11.2%;	Score 116.4;	DB 7;	Length 1480;
	Best Local Similarity	57.4%;	Pred. No. 9.le-11;		
	Matches 263;	Conservative 0;	Mismatches 171;	Indels 24;	Gaps
QY	137	CCGCTGCTGGCCCAAGGCCCGGAGGGGCCTGGGNAACCGGCATGCGGTGTACTTGGAAAC	196		
Db	92	cctccttgggtgctgtgcagtcgtggccgctgctgatcgccacaccgtctcttcygaac	151		
QY	197	AGTGTCAACACGACACTGCGGGCAGAGGGCTACACCCTGCAGGTGAACGTGAACGACTAT	256		
Db	152	agtccaattcccgaatgccggactcacaccatacatgtgcagctgtaatgactac	211		
QY	257	CTGGATTATTTACTGCCCGCACTACAACAGCTCGGGGTGGCCCCGGCGGGGACCGGGG	316		
Db	212	gtggacatcatctgtccgcacctatgaagatacactctgtggagaagctgcgatg-----	265		
QY	317	COCGGAGGCGGGCAGACGAGTACGTGCCTTACATGTGTAGCGCGCAACCGGCTACCGCAC	376		
Db	266	-----gagcagtatcatactgtaccctgtgtaggcatgaggatcaccagctg	310		
QY	377	TGCAACGCCAG---CCAGGGCTTTCAGCGGTGGGAGTGCACCGGCCGCACGCCGCCGCAC	433		
Db	311	tgcagccccaqtfccaaagdaccaaatccctgtgcaatgcaacccgcccgaatgccaaagct	370		







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Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	901	86.9		1030	9	AL533153	AL533153 AL533153
2	649.6	62.6		804	10	BF983120	BF983120 602305829
3	615.6	59.4		684	9	AL527972	AL527972 AL527972
4	553.2	53.3		902	9	AL546822	AL546822 AL546822
5	438.2	42.3		496	10	BF963157	BF963157 CM3-NN118
6	421.4	40.6		884	10	BG705182	BG705182 602688106
7	409	39.4		535	9	AW785993	AW785993 120664 MA
8	363.8	35.1		702	10	BG743158	BG743158 602634316
9	322.2	31.1		848	10	BF542148	BF542148 602068243
10	289.6	27.9		552	9	AL628407	AL628407 AL628407
11	268.4	25.9		879	10	BF977204	BF977204 602146759
12	257.8	24.9		460	9	AW200648	AW200648 da24c06.y
13	247.8	23.9		1013	10	BF969747	BF969747 602272160
14	246.2	23.7		288	9	AA338749	AA338749 EST43752
15	220.2	21.2		258	10	BF950361	BF950361 CM3-NN118
16	217.4	21.0		750	9	AW199923	AW199923 da24c06.x
17	217.4	21.0		906	10	BF240606	BF240606 601875729



BASE COUNT	146 a	203 c	199 g	94 t	42 others
ORIGIN					
Query Match	59.4%;	Score 615.6;	DB 9;	Length 684;	
Best Local Similarity	89.3%;	Pred. No. 2.6e-90;			
Matches 609; Conservative	42;	Mismatches 31;	Indels 0;	Gaps	
Qy	112	GCTGCTGCGCCGTCGCGCTGCTGCGCTGCTGCGCCAAAGGCGCCGAGGGCGCGCTGGG	171		
Db	1	GCTGCTGCTGCMGTCGCGCTGCTGCCAGCTGCTGCGCCCAAGGGCCCGGAGGGCGAAGG	60		
Qy	172	AAACCGGCATGCGGTGTACTGGAACAGCTCCAAACACGACCTCGCGCGAGAGGGCTACAC	231		
Db	61	AAACMGCGATGCGGTGTACTGGAACARCMWCCAACGACACCTCGCGCGAGAGGGCWACAM	120		
Qy	232	CGTGCAGGTGAAGCTGAACAGCACTATCTGGATATTTACTGCCCGCACTACAAACAGCTCGGG	291		
Db	121	MAAGMAGGTGAAGCTGAACAGCACTATTTGGATATWMAAAGACGMAAMTAAANMAGCWGGG	180		
Qy	292	GGTGGGCCCCGGGCGGGACCGGGGCCCGGAGCGGGGAGAGAGCTACTGCTGCTGTACAT	351		
Db	181	GGTRGGCCCCGGGCGGGAGMCGGGGCCCGGAGCGGGGCGGCGARCACTAGTCTGTACAT	240		
Qy	352	GGTGAGCGCAAGCGGTACCGCACCTGTCACAGCCAGCCAGGGCTTCAAGCGCTGGGAGTG	411		
Db	241	GGWGAGCMGCAACGGCWACMGCACCTGCCACAGCCAGCAAGGGCTTMAAGCGCTGGGAGTG	300		
Qy	412	CAACGGCGCGAGCCGCCGCACAGCCCCATCAAGTTCTCGGAGAGTTTCCAGGCGTACAG	471		
Db	301	CAACGGCGCGACGCMCGCMGAMAGCCCCATMAAGTTCTCGGAGAAGTTCCAGCGCWAAAR	360		
Qy	472	CGCCTTCTCTGGGTACAGTTCCACGCCGCGCCACGAGTACTACTACATCTCCACGCC	531		
Db	361	CGCCTTCMTCTGGCGWACCAGTWCACGCMGCGCCACGAGTACTACWAMATCTCCACGCC	420		
Qy	532	CACTCACAACCTGCACCTGGAAGTGTCTGAGGATGAAGGTGTTCTGCTGTGGCGCTCCAC	591		
Db	421	CACTCAMAACCTGCATCTGGAAGTGTCTGARGATGAAGGTGTTCTGCTGCAGCGCTCCAC	480		
Qy	592	ATCGCATCCGGGGAGAACCGGTCGCCACTCTCCGCCAGTTTCAACATGGGCCCCCAATGT	651		
Db	481	ATCGCATCCGGGGAGAACCGGTCGCCACTCTCCGCCAGTTTCAACATGGGCCCCCAATGT	540		
Qy	652	GAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCTCAGTGCGCCAAGCTTGAGAA	711		
Db	541	GAAGATMAACGTGCTGGAAGACTTTGAGGGAGAGAACCTCAGTGCGCCAAGCTTGAGAA	600		
Qy	712	GAGCATCAGGGGACACAGCCCCAAACGGGAACACCTTGCCCTGGCCGTGGGCATCGCCCT	771		
Db	601	GAGCATCAGGGGACACAGCCCCAAACGGGAACACCTTGCCCTGGCCGTGGGCATCGCCCT	660		
Qy	772	CTTCCTCATGACGTTCTTTGGCC	793		
Db	661	CTTCCTCMGACGATCTTGGC	682		

RESULT	4
AL546822	
LOCUS	902 bp mRNA linear EST 16-FEB-2001
DEFINITION	AL546822 LTI_NFL006_Pf.2 Homo sapiens cDNA clone CS0DI026YI24 5 prime, mRNA sequence.
ACCESSION	AL546822
VERSION	AL546822.1 GI:12880311
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)

COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
source 1..902  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DI026YI24"  
/clone\_lib="LRI.NFL006.PL2"  
/tissue\_type="placenta"  
/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end cloned, double-stranded cDNA was digested with Not I and inserted into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 161 a 297 c 278 g 156 t 10 others  
ORIGIN

Query Match 53.3%; Score 553.2; DB 9; Length 902;  
Best Local Similarity 91.1%; Pred. No. 3.3e-80;  
Matches 749; Conservative 8; Mismatches 37; Indels 28; Gaps 15;

QY 201 CCAACACGACCTCGCGGAGAGGCTACACGCTGCAGTGAACTGAA-----CGA 252  
Db 67 CCCACGCTCGCGGAGACGACGCGCTACACGCTGCAGTGAACTGAGAGAGCTCAC 126

QY 253 CTATCTGGATATTACTGCCGCACTACAACAGCTCGGGGTGGCCCGGGGGCGG--G 309  
Db 127 TGGTGGATATGTAGTCTGCCGCACTACACAGCTCGGGGTGGCCCGGGGGCGGAC 186

QY 310 ACCGGGGCGGAGCGGGGCGAGA--GCAGTAGG--TGCTGTAG--ATGTTGAGCGGCAACGG 366  
Db 187 CGCGGGCGGCGGAGCGGCGAGCGCAGTACGCTGCTGTAGATGTTGAGCGCAACGG 246

QY 367 CTACCGCACTTCAACGCGCAGCGGCTTCAAGCGCTGGAGTGCACCGCGCGCAGCG 426  
Db 247 CTACCGCACTTCAACGCGCAGCGGCTTCAAGCGCTGGAGTGCACCGCGCGCAGCG 306

QY 427 CCGGCACAGCCCAT--CAAGTTCTCGGAGAGTTCCAGCGGTACA--CGCGCTTCTCTCT 483  
Db 307 CCGGCACAGCCCATGCAAGTTCTCGGAGAGTTCCAGCGGTACAGCGCGGCTTCTCT 366

QY 484 GGGCTACGAGTTCCAGCGGCGCAGAGTACTACTACATCTCCAGCGCCCACTCAACCT 543  
Db 367 GGGCTACGAGTTCCAGCGGCGCAGAGTACTACTACATCTCCAGCGCCCACTCAACCT 426

QY 544 GCACCTGAAGTGTCTGAGATGAAGTGTCTGCTGCTGCGCTCCACATCGCACTCCGG 603  
Db 427 GCACCTGAAGTGTCTGAGATGAAGTGTCTGCTGCTGCGCTCCACATCGCACTCCGG 486

QY 604 G-GAGAAGCGGTCCTCCCACTCTCCCGGAGTTCAACATGGGCGCCCAATGTGAAGATCAACG 662  
Db 487 GCGAGAAGCGGTCCTCCCACTCTCCCGGAGTTCAACATGGGCGCCCAATGTGAAGATCAACG 546

QY 663 TGCTGGAAGACTTTGAGGAGAGAACCTCAGGTGCCCAAGCTTGAGAAGAGCAT--CAG 720  
Db 547 TGCTGGAAGACTTTGAGGAGAGAACCTCAGGTGCCCAAGCTTGAGAAGAGCATGCAAG 606

QY 721 CGGGACACGCCCCAACGGGACACCTGCGCTGCGCTGGCATCGCTTCTTCTCAT 780  
Db 607 CGGGACACGCCCCAACGGGACACCTGCGCTGCGCTGGCATCGCTTCTTCTCAT 666

QY 781 GACGTTCTTGGCCTCTAGCTCTGCGCCCTCCCTT--GGGGGGGAGAGATGGGGGGGGC 839  
Db 667 GACGTTCTTGGCCTCTAGCTCTGCGCCCTCCCTT--GGGGGGGAGAGATGGGGGGGGC 726

QY 840 TTGGAAGAGGAGGAGGAGCGCTTTGGCGCTCTCCAAGGGAAGCCCTAGTGGCCCTAGACCCCTC 899  
Db 727 TTGGAAGAGGAGGAGGAGCGCTTTGGCGCTCTCCA--GGAARCCCTAGTGGGCTAGA--CCCTC 784

QY 900 CTCCTCATGGCTAGAGTGGGCGCTGCACCATACATCTGTCCGCCCTCTACCCCTTC 959  
Db 785 CTCCTCATGGCTAGAGTGGGCGCTGCACCATACATCTGTCCGCCCTCTACCCCTTC 841

QY 960 CCCCCACCTAGGCGACTCTAGTGGACCAAGCACGGGACAGC 1001  
Db 842 CCCCCACCTA--GGCACTCTAGTGA--CAAGCACGGGACAC 881

RESULT 5  
BF953157/c  
LOCUS BF953157 496 bp mRNA linear EST 22-JAN-2001  
DEFINITION CM3-NN1187-111100-478-a06 NN1187 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF953157  
VERSION BF953157.1 GI:12370432  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 496)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3at2-CM3-NN1187-111100-478-a06&t3=2000-11-11&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 19  
High quality sequence stop: 495.  
Location/Qualifiers  
source 1..496  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NN1187"  
/dev\_stage="Adult"  
/note="Organ: nervous\_normal; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 94 a 144 c 162 g 96 t  
ORIGIN

Query Match 42.3%; Score 438.2; DB 10; Length 496;  
Best Local Similarity 97.9%; Pred. No. 1.2e-61;  
Matches 465; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 539 AACCTGCACTGGAGTGTCTGAGATGAAGTGTGCTGCTGCGCTCC--ACATCCGA 597  
|||||







```

Db 301 TACCCCTTCCCCACGTAGGGCACTGTAGTGACCAAGCACGGGACACCCATGGGTCC 360
QY 1011 CGAGCAG 1017
    || || |
Db 361 CGGGCGG 367

RESULT 9
BF542148      848 bp mRNA linear EST 11-DEC-2000
LOCUS 602068243F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067314 5',
DEFINITION mRNA sequence.
ACCESSION BF542148
VERSION BF542148.1 GI:11629529
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapps@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM906 row: e column: 11
High quality sequence stop: 511.
Location/Qualifiers
    1..848
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:4067314"
    /clone_lib="NIH_MGC_58"
    /tissue_type="hypernephroma"
    /lab_host="DH10B (11 phage-resistant)"
    /note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1:
    SfiI (ggcgctcgcc); Site_2: SfiI (ggcgattggcc);
    Double-stranded cDNA was prepared from cell line RNA. 5'
    and 3' adaptors were used in cloning as follows: 5'
    adaptor sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor
    sequence: 5'-ATTCTAGAGCGCGGCGGCGGACATG-dt(30)BN-3'
    (where B = A, C, or G and N = A, C, G, or T). Average
    insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
    contained inserts by PCR. This library was enriched for
    full-length clones and was constructed by Clontech
    Laboratories (Palo Alto, CA)."
BASE COUNT 175 a 238 c 282 g 153 t
ORIGIN

Query Match 31.1%; Score 322.2; DB 10; Length 848;
Best Local Similarity 89.0%; Pred. No. 7.4e-43;
Matches 462; Conservative 0; Mismatches 43; Indels 14; Gaps 10;

QY 509 GAGTACTACTACATCTCCAGCGCCACTCAACACTGCACCTGGAGTGTCTGAGGATGAAG 568
    ||| | |||
Db 105 GAGATCGCTGTTTCTCCAGCGCCACTCAACACTGCACCTGGAGTGTCTGAGGATGAAG 164

QY 569 GTGTTGCTGCTGCGGCTCCACATCGCACTCCGGGGAGAGCGGTGCCCACTCTCCCCC 628
    ||| | |||
Db 165 GTGCTGCTGCTGCGGCTCCACATCGCACTCC-GGAGAGCGGTGCCCA-TCCTCCC 221

QY 629 CAGTTACCATGGGCCCCCAATGTGAGATCAACGTGCTGGAAGACTTTGAGGAGAGAAC 688
    ||| | |||
Db 222 CAGTTACCATGGGCCCCCAATGTGAGATCAACGTGCTGGAAGACTTTGAGGAGAGAAC 189

```

```

QY 689 CCTAGGTGCCCAAGCTTGAGAGAGCATCAGCGGACACGCCCAAGCGGGAAACACCTG 748
    ||| | |||
Db 282 CCTAGGTGCCCAAGCTTGAGAGAGCATCAGCGGACACGCCCAAGCGGGAAACACCTG 341
    ||| | |||
QY 749 CCCTTGGCGGTGGGCATCG-CCTTCTCTCTCATGAGTCTT-TGGCCTCCTAGCTCT-CC 805
    ||| | |||
Db 342 CCCTTGGCGGTGGGCATCGCCCTTCTCTCATGAGTCTTCTAGGCGCTCCTAGCTCTGGC 401
    ||| | |||
QY 806 CCCTTCCCTGGGGGGGAGAGATGGGGGGGCTTTGGAAGGAGCAGGGA-GCCTTTTGGC 864
    ||| | |||
Db 402 CCCTTCCCTGGGGGGGAGAGATGGGGGGGTTTGAAGGAGCAGGATGCTTTGGG 461
    ||| | |||
QY 865 CTCTCCAAGGAAAGCCTAGTGGGCTTAGACCCCTCTCCCATGCTAGAGTGGGCGCTG 924
    ||| | |||
Db 462 CTCTCCAAGGAAAGCCTAGTGGGCTTAGAGCCCTCTCCCATG-TAGAAGTGGGCGCTG 520
    ||| | |||
QY 925 CACCATAACA---TCTGTGTCGGCCCTCTACCCCTTCCCCCAGTAGGGCAC---TGT 978
    ||| | |||
Db 521 AACCATACAACTGTGTCTCGCCCTTTTAAACATTTCACCCACCTAGGGCACCTGTGT 580
    ||| | |||
QY 979 AGTGGACCAAGCACGGGACGACCATGGGTCCCGAGCAG 1017
    ||| | |||
Db 581 AGTGGACCAAGCACGGGACGACCAATGGTCTCCGGGGCGG 619
    ||| | |||

RESULT 10
AL628407      552 bp mRNA linear EST 02-NOV-2001
LOCUS AL628407 XCC-gastrula Silurana tropicalis cDNA clone TGas008p08 5',
DEFINITION mRNA sequence.
ACCESSION AL628407
VERSION AL628407.1 GI:16597890
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
    1 (bases 1 to 552)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E.
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas008p08.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
    1..552
    /organism="Silurana tropicalis"
    /db_xref="taxon:8364"
    /clone="TGas008p08"
    /clone_lib="XCC-gastrula"
    /dev_stage="gastrula (stages 10-5-13 mixed)"
    /lab_host="Escherichia coli XL1-blue"
    /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
    was oligo dt primed from Sug of poly A+ RNA from stages
    10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
    into pCS107 with EcoRI at the 5' end and NotI at the 3'
    end."
BASE COUNT 123 a 186 c 138 g 104 t 1 others
ORIGIN

Query Match 27.9%; Score 289.6; DB 9; Length 552;
Best Local Similarity 72.9%; Pred. No. 1.3e-37;
Matches 398; Conservative 0; Mismatches 124; Indels 24; Gaps 1;

QY 130 GCTGCTCCGCTGCTGGCCCAAGGGCGCGGAGGGCGCTGGGAAACCGGCATGCGGTGTA 189

```



Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Library constructed by Bruce Blumberg  
Library normalized by Jihwan Song  
DNA Sequencing by: Washington University Genome Sequencing Center.  
Clone distribution: Xenopus clone distribution information for  
this library can be found through Research Genetics, visit their  
web page at: <http://www.resgen.com/>  
Seq primer: -40RP from Gibco  
High quality sequence stop: 423.

## FEATURES

## Source

1. 460  
/organism="Xenopus laevis"  
/db\_xref="taxon:8355"  
/clone="XENOPUS\_SOURCE\_ID:xlnga003n11"  
/tissue\_type="gastrula (stages 10.5, 11.5 mixed)"  
/lab\_host="Top-10 F"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was prepared from 2ug of poly A+ RNA (equal  
parts from stage 10.5 and stage 11.5 gastrulae).  
EcoRI-XhoI cut cDNA was then ligated into Unizap-XR  
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'  
end. SS-library phagemids were prepared by mass excision  
from the original library and normalized by hybridization  
to biotinylated driver (prepared from the same library by  
PCR) to Cot-omega of 11. After removal of hybrids and  
excess driver by streptavidin sepharose chromatography,  
the ss-phagemids were made double stranded and  
electroporated into Top-10 F'. Original library  
construction by Bruce Blumberg (Cho et al. 1991 Cell 67,  
1111-1120). Normalized by Jihwan Song (Song, Cho and  
Blumberg, unpublished). Note: This is a Xenopus Gene  
Collection (XGC) library." 93 t

BASE COUNT 118 a 139 c 110 g 93 t

ORIGIN

Query Match 24.9%; Score 257.8; DB 9; Length 460;

Best Local Similarity 74.0%; Pred. No. 1.7e-32;

Matches 344; Conservative 0; Mismatches 112; Indels 9; Gaps 1;

QY 332 GAGCAGTACCTGCTGTACATGGTACCGCGGACGCGCTACCGACCTCGACGCGCCAGCAG 391

Db 5 GAGCAGTACATCTCTATATGGTACGAGGCTACCGGACCTCGACATCAGCCAG 64

QY 392 GGCTTCAAGCGCTGGAGTGCACCGCGCCGACCGCCGACCGCCATCAAGTTCTCG 451

Db 65 GGCTTCAAGCGCTGGAGTGTACCGCGCCGACCGCTACCGACAGTCCAAATCAATCTCC 124

QY 452 GAGAAATTCCAGCGCTACAGCGCTTCTCTCTGGGCTACGAGTTCCACGCGCGCCAGAG 511

Db 125 GAGAAATTCCAGCGGTACAGCGCTTCTCTCTGGGCTACGAGTTCCACGCGCGCCAGAG 184

QY 512 TACTACTACATCTCCAGCGCCACTCAACCTGCACCTGGAGTGTCTGAGATGAAGGTG 571

Db 185 TACTACTATATCTGACACCGGACCAATCAACAGCGGCTCTGTCTGAAGAAGAAAGT 244

QY 572 TTGCTCTGCTGGCGCTCCACATCGACTCCGGGAGAGCGGTGCCACTCTCCCGCCAG 631

Db 245 TTGTGTGTGCGCCAGCACTCCACTCCGGAGAGAAATCTCCCGACCTCCCGCCAG 304

QY 632 TTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCTT 691

Db 305 TTCAGATAGGCGCCAGAGGTCAACATAGAGGATTTAGATAACTT-----CAACCCG 355

QY 692 CAGGTGCCCCAAGCTTGAGAGAGCATCAGCGGACAGCGCCCAACCGGGAACACCTCCCC 751

Db 356 GAGATCCCAAGTTGGAGAGAGCGTCAAGTGGGAGCAGTCCCAAAAGGAAGCACTTACAC 415

QY 752 CTGGCGGTGGGCTCGCTTCTCTCATGACGTTCTTGGCTCC 796

Db 416 TTACAGTTCGAGTTGCTCTCTCTATTAATGACGCTCTGGCTTCC 460

## RESULT 13

BF969747

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF969747 1013 bp mRNA linear EST 22-JAN-2001  
602272160F1 NIH\_MGC\_84 Homo sapiens cDNA clone IMAGE:4360358 5',  
mRNA sequence.  
BF969747  
BF969747.1 GI:12336962  
EST.  
human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1013)

NIH-MGC 1 to 1013

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM10001 row: g column: 15

High quality sequence stop: 715.

Location/Qualifiers

1. 1013

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4360358"

/clone\_lib="NIH\_MGC\_84"

/tissue\_type="adrenal cortex carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site\_1:

NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dT

primed. Average insert size 1.229 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

234 a 293 c 285 g 200 t 1 others

BASE COUNT

ORIGIN

Query Match 23.9%; Score 247.8; DB 10; Length 1013;  
Best Local Similarity 98.5%; Pred. No. 8.2e-31;  
Matches 271; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 744 ACCTGCCCCCTGGCGGTGGGCATCGCCTTCTTCTCATGACGCTTCTTGGCCCTCCTAGCTCT 803

Db 1 ACCTGCCCCCTGGCGGTGGGCATCGCCTTCTTCTCATGACGCTTCTTGGCCCTCCTAGCTCT 60

QY 804 GCCCCTTCCCTT-CGGGGGGGAGAGATGGGGGGGCTTGAAGGAGCAGGAGCCTTTG 862

Db 61 GCCCCTTCCCTTGGGGGGGAGAGATGGGGGGGCTTGAAGGAGCAGGAGCCTTTG 120

QY 863 GCCTCTCAAGGGAAGCCTAGTGGCCTAGACCCCTCTCTCCCATGGCTAGAAAGTGGGGCC 922

Db 121 GCCTCTCAAGGGAAGCCTAGTGGCCTAGACCCCTCTCTCCCATGGCTAGAAAGTGGGGCC 180

QY 923 TGACCATACATCTGTGTCCGCCCTTCTTACCCCTTCCCCACAGTAGGGCAGCTGTAGTG 982

Db 181 TGACCATACATCTGTGTCCG-CCTCTTACCCCTTCCCCACAGTAGGGCAGCTGTAGTG 239

QY 983 GACCAAGCAGGGGACAGCCCATGGTCCCGAGAG 1017

Db 240 GACCAAGCAGGGGACAGCCCATGGTCCCGAGAG 274

## RESULT 14

AA338749

**LOCUS** AA338749 288 bp mRNA linear EST 21-APR-1997  
**DEFINITION** EST43752 Fetal brain I Homo sapiens cDNA 5' end similar to similar  
to tyrosine kinase receptor, mRNA sequence.  
**ACCESSION** AA338749  
**VERSION** AA338749.1 GI:1991007  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 288)  
**AUTHORS** Adams M.D., Soares M.B., Kerlavage A.R., Fields C. and Venter J.C.  
**TITLE** Rapid cDNA sequencing (expressed sequence tags) from a  
directionally cloned human infant brain cDNA library  
**JOURNAL** Nature Genet. 4, 373-380 (1993)  
**MEDLINE** 94004965  
**COMMENT** Other ESTs: EST43751  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD, 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
**FEATURES** Location/Qualifiers  
source  
1..288  
/organism="Homo sapiens"  
/db\_xref="ATCC (Inhost):102467"  
/db\_xref="taxon:9606"  
/clone\_lib="Fetal brain I"  
/sex="female"  
/dev\_stage="fetus, 24 wks"  
/notes="Organ: brain; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI"  
**BASE COUNT** 63 a 89 c 82 g 54 t  
**ORIGIN**  
Query Match 23.7%; Score 246.2; DB 9; Length 288;  
Best Local Similarity 96.9%; Pred. No. 1.2e-30;  
Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 509 GAGTACTACTACATCCACGCGCCACTCACACCTGCACCTGGAAGTGTCTGAGGATGAAG 568  
||| |||  
Db 30 GAGATCGCTGTTCTCCACGCCCACTCACACCTGCACCTGGAAGTGTCTGAGGATGAAG 89  
QY 569 GTGTTGCTGCTGCGCTCCACATCGCACTCCGGGAGAGCGCGTCCCACTCTCCCC 628  
||| |||  
Db 90 GTGTTGCTGCTGCGCTCCACATCGCACTCCGGGAGAGCGCGTCCCACTCTCCCC 149  
QY 629 CAGTTACCATCGGGCCCAAGTGAAGATCAACGTCCTGGAAGACTTTGAGGGAGAGAAC 588  
||| |||  
Db 150 CAGTTACCATCGGGCCCAAGTGAAGATCAACGTCCTGGAAGACTTTGAGGGAGAGAAC 209  
QY 689 CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGGACAGCCCAACACGGAACACCTG 748  
||| |||  
Db 210 CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGGACAGCCCAACACGGAACACTG 269  
QY 749 CCCCTGGCCGTGGGCATCG 767  
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Db 270 CCCCTGGCCGTGGGCATCG 288  
**RESULT** 15  
BF950361 258 bp mRNA linear EST 22-JAN-2001  
**LOCUS** BF950361  
**DEFINITION** CM3-NN1187-041100-465-c09 NN1187 Homo sapiens cDNA, mRNA sequence.  
**ACCESSION** BF950361  
**VERSION** BF950361.1 GI:12367636

**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 258)  
**AUTHORS** Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,  
Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,  
Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H.,  
Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare  
M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and  
Simpson A.J.J.  
**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**MEDLINE** 20202663  
**COMMENT** Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-NN1187-041100-465-c09&t3=2000-11-04&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 12  
High quality sequence stop: 258.  
**FEATURES** Location/Qualifiers  
source  
1..258  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NN1187"  
/dev\_stage="Adult"  
/notes="Organ: nervous\_normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
**BASE COUNT** 51 a 85 c 78 g 43 t 1 others  
**ORIGIN**  
Query Match 21.2%; Score 220.2; DB 10; Length 258;  
Best Local Similarity 98.3%; Pred. No. 1.9e-26;  
Matches 233; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 612 CGGTCCCACTCTCCGCCAGTTCCACATGGGCCCCCAATGTGAAGATCAACGTGCTGGAAG 671  
||| |||  
Db 23 CGGTCCCACTCTCCGCCAG-TCACCATGGGCCCCCAATATGAAGATCAACGTGCTGGAAG 81  
QY 672 ACTTTGAGGAGAGAACCCCTCAGTGCCTCAGTTGAGAGAGCATCAGCGGACCGCC 731  
||| |||  
Db 82 ACTTCGAGGAGGAGAACCCCTCAGTGCCTCAGTTGAGAGAGCATCAGCGGACCGCC 141  
QY 732 CCAACGGAACACCTGCCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGAGTTCTTGG 791  
||| |||  
Db 142 CCAACGGAACACCTGCCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGAGTTCTTGG 201  
QY 792 CCTCTAGCTCTGCCCCCTCCCTCGGGGGGAGAGATGGGGCGGGCTTGAAGGA 848  
||| |||  
Db 202 CCTCTAGCTCTGCCCCCTCCCTCGGGGGGAGAGATGGGGCGGGCTTGAAGGA 258

Search completed: September 27, 2002, 22:03:08  
Job time: 6594 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 27, 2002, 22:43:05 ; Search time 74.08 Seconds  
(without alignments)  
356.852 Million cell updates/sec

Title: US-09-904-954-2

Perfect score: 1301

Sequence: 1 MAAPLLLLLLLLVPVPLP.....REHPLAVGIAFFLMTFLAS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	100.0	238	16	AA1981 Human hek-L protei
2	1266	97.3	234	16	AA1982 Eph transmembrane
3	437	33.6	209	17	AA1983 Mouse Eph receptor
4	437	33.6	209	19	AA1984 Amino acid sequenc
5	437	33.6	213	20	AA1985 Human LERK-6 polyp
6	426.5	32.6	335	22	AA1986 Novel human diagno
7	421	32.4	200	17	AA1987 Chicken Eph recept
8	421	32.4	200	19	AA1988 Amino acid sequenc
9	415.5	31.9	228	17	AA1989 Human AL-1, a liga
10	415.5	31.9	228	17	AA1990 Lerk-7 protein. H
11	415.5	31.9	228	17	AA1991 HEK4 binding prote

12	403	31.0	184	17	AA1992 Lerk-6 protein. M
13	403	31.0	184	17	AA1993 LERK-6 protein. M
14	403	31.0	184	20	AA1994 Murine LERK-6 poly
15	390	30.0	205	13	AA1995 B61 protein sequen
16	390	30.0	205	15	AA1996 EBP. Homo sapiens
17	390	30.0	205	16	AA1997 Eph transmembrane
18	390	30.0	205	18	AA1998 eck receptor bindi
19	386	29.7	205	22	AA1999 Human PRO202 prote
20	386	29.7	218	21	AA2000 Human pancreatic c
21	384	29.5	180	18	AA2001 AAB54058
22	382	29.4	171	18	AA2002 AAB54058
23	380	29.2	167	18	AA2003 Truncated eck rece
24	379.5	29.2	160	18	AA2004 Truncated eck rece
25	377.5	29.0	151	18	AA2005 Truncated eck rece
26	377.5	29.0	204	22	AA2006 Human PRO202 polyp
27	377.5	29.0	204	22	AA2007 Human PRO202 prote
28	364.5	28.0	179	19	AA2008 EPH receptor ligan
29	364.5	28.0	179	19	AA2009 Generic sequence f
30	364.5	28.0	201	16	AA2010 Human hek-L protei
31	334	25.7	104	17	AA2011 LERK-6 exon polype
32	334	25.7	104	20	AA2012 Amino acid sequenc
33	295	22.7	58	21	AA2013 Human secreted pro
34	180	13.8	340	18	AA2014 EPH family ligand
35	180	13.8	340	19	AA2015 Human transmembran
36	179	13.8	340	18	AA2016 AL-2-short (AL-2s)
37	179	13.8	340	18	AA2017 Human cytokine Ler
38	179	13.8	340	18	AA2018 NLERK2 ligand for
39	179	13.8	455	18	AA2019 AL-2-long (AL-2l)
40	177	13.6	658	21	AA2020 Ephrin-B2-Ephrin-B
41	171.5	13.2	308	17	AA2021 Ligand #2 for rece
42	171.5	13.2	308	17	AA2022 Ligand for recepto
43	171.5	13.2	333	17	AA2023 Full length ligand
44	171.5	13.2	333	17	AA2024 Ligand for recepto
45	171.5	13.2	333	17	AA2025 Human hepatoma tra

ALIGNMENTS

RESULT	1
AA1981	AA1981
ID	AA1981 standard; Protein; 238 AA.
XX	AA1981
AC	AA1981
DT	03-OCT-1995 (first entry)
XX	Human hek-L protein.
DE	Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
KW	Immunogen.
XX	Homo sapiens.
OS	Homo sapiens.
XX	Key
FH	Location/Qualifiers
FT	Peptide
FT	1..19
FT	/note= "signal peptide"
FT	Protein
XX	20..238
XX	WO9506065-A.
PN	WO9506065-A.
XX	02-MAR-1995.
PD	02-MAR-1995.
XX	17-AUG-1994;
XX	94WO-US09282.
XX	20-AUG-1993;
PR	93US-0109745.
PR	30-AUG-1993;
PR	93US-0114426.
PR	03-DEC-1993;
PR	93US-0161132.
PR	09-MAY-1994;
PR	94US-0240124.
XX	(IMMV ) IMMUNEX CORP.
PA	Beckmann MP, Cerretti DP;
XX	
PI	

PF	04-APR-1995;	95WO-US04208.
XX		
PR	21-OCT-1994;	94US-0327423.
PR	04-APR-1994;	94US-0222075.
PR	12-APR-1994;	94US-0229402.
PR	01-SEP-1994;	94US-0299567.
XX	(REGE-) REGENERON PHARM INC.	
PA	Aldrich TH, Davis S, Gale N, Goldfarb M, Maisonnier PC;	
XX	Yancopoulos GD;	
PI	WPI; 1995-358635/46.	
XX	N-PSDB; AAT03883.	
DR	Ligands which bind Eph family receptors - used in the diagnosis of neurological disorders	
PT	Disclosure; Fig 2; 58pp; English.	
XX		
PS	Efl-2 (also known as EHK-1L) is an Eph transmembrane tyrosine kinase family ligand. It has homology with Bcl (Efl-1) (see AAR82604). Efl-2 ends in a C-terminal hydrophobic sequence that appears to be a recognition sequence allowing it to be GPI-linked and thus lacking in an intracellular domain. Efl-2 is useful for identifying other ligands of Ephk-1, -2, -3, Eck and Elk receptors. The ligands are useful in promoting a differential function and/or influencing the phenotype, such as growth and/or proliferation, of receptor bearing cells. They may be used in the diagnosis, and treatment of neurological disorders.	
XX		
SQ	Sequence	234 AA;
Query Match 97.3%; Score 1266; DB 16; Length 234;		
Best Local Similarity 98.3%; Pred. No. 2.8e-120;		
Matches 234; Conservative 0; Mismatches 0; Indels 4; Gaps		
Qy	1	MAAAPLLLLLLVPVPLLPALLAQGGGALGNRHAYVNSSNOHLREGVTQVNVNDYLD 60
Db	1	maaaPLLLLLLLvpvpllpallagpggaglnrhayvnssnqhlrregvtqvnvndyl d 60
Qy	61	IYCPHYNSSGVGPAGPGGGGAEQVLVYMVRNGYRTCNASQGPKRWECNRPHAPHSP I 120
Db	61	iycphyNSS---ga gpgpggaeqyvlymvrngyrtnasqgfkrcwecnrphaphsp i 116
Qy	121	KFESEKQRYSAFSLGSIEFHAGHEYYIYSTHNLHWKCLRMKFVCCASTSHSGEKPVPT 180
Db	117	kfesekfryrsatsfyefhagheyyisctphnlhwkclrmkfvrccastshsgekpvpt 176
Qy	181	LPQFTMGPNVKINLVDFEGENQPVPKLKSISGTSRKREHLPLAVGIAFFLMTFAS 238
Db	177	lpqftmgpnvkinvldefegenqpvpkleksisgtspkrehlplavgiafflm tflas 234
RESULT 3		
ID	AAR94766	
XX	AAR94766 standard; Protein; 209 AA.	
XX	AAR94766;	
XX		
DT	02-JUL-1996 (first entry)	
XX		
DE	Muscle EPH receptor ligand Elf-1.	
XX		
KW	Elf-1; EPH receptor ligand; dementia; tachycardia; therapy; diagnosis; transgenic animal.	
KW		
OS	Mus musculus.	
XX		
FH	Key Location/Qualifiers	
FT	Peptide 1..20	
FT	/label= Sig_peptide	
FT	Protein 21..209	

DT	20-OCT-1998	(first entry)
XX		
XX		
KW	Amino acid sequence of a mammalian Elf-1 protein.	
KW		
KW	Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation.	
KW		
KW		
OS	Mus sp.	
XX		
XX		
Key	Location/Qualifiers	
FF	Peptide	1..20
FT		/note= "signal peptide"
FT	Protein	21..209
FT		/note= "mature protein"
FT	Modified-site	38
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	35..166
FT		/note= "contains core sequence motif"
FT	Misc-difference	69..159
FT		/note= "contains a Cys4 motif"
FT	Modified-site	170
FT		/note= "potential N-linked glycosylation site"
FT	Modified-site	184
FT		/note= "potential N-linked glycosylation site"
XX		
XX	US5795734-A.	
PN		
XX		
XX	18-AUG-1998.	
PD		
XX		
XX	31-MAY-1995;	95US-0455001.
PF		
XX		
PR	31-MAY-1995;	95US-0455001.
PR	19-SEP-1994;	94US-0308814.
PR	27-FEB-1995;	95US-0393462.
XX		
XX	(HARD ) HARVARD COLLEGE.	
PA		
XX		
XX	Cheng H, Flanagan JG;	
PI		
XX		
XX	WPI; 1998-466665/40.	
DR	N-PSDB; AAV42926.	
DR		
XX		
PT	Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor	
PT	- for production of Elf-1 protein, useful for regulating	
PT	proliferation, differentiation, and survival of cells	
XX		
XX	Claim 1; Fig 2A; 53pp; English.	
PS		
PS		
XX		
CC	The present sequence represents a mammalian EPH receptor ligand	
CC	designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is	
CC	a tyrosine kinase ligand, which is linked to the membrane through a	
CC	phosphatidylinositol linkage. It shares some homology to 2 other EPH	
CC	receptor ligands, B61 and LERK-2. The Elf-1 protein modulates	
CC	proliferation, differentiation and survival of EPH receptor-expressing	
CC	cells by stimulating or antagonising intracellular signalling mediated	
CC	by the EPH receptor. Typical of many potential applications are	
CC	increasing survival of neuronal cells in culture (e.g. where intended for	
CC	transplantation), also therapeutically in increase neuron survival	
CC	(e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent	
CC	nervous system and lymphatic tumours, to induce differentiation of	
CC	hepatocytes to form an artificial liver, to induce cartilage and bone	
CC	formation.	
XX		
XX		
SQ	Sequence	209 AA;

Query Match 33.6%; Score 437; DB 19; Length 209;  
 Best Local Similarity 50.5%; Pred. No. 3.6e-36;  
 Matches 96; Conservative 25; Mismatches 47; Indels 22; Gaps 7;

QY 2 AAAPLLLLLLVPLPPLA--QGPGGALGNRHAVYWNSSNOHLRR-----GYTVQV 53  
Db 4 adrpilpllll-----llpirarnedparanadryavymrnsprfqvsavggdytvev 59  
QY 54 NYNDYLDIYCPHNSGVGPGGAGPGGAEQVLYVMVSRNGYRTCNASQ-GFKRWEKNR 112  
Db 60 sindyldiycphy-----gaplpaermerlylmvngvghascdhrqgrfkrwechr 112  
QY 113 PHAPSPIKFEKFORYSAFSLGYEFHAGHEYYIIS-TPTHNLHWKCLRMKVFVCCAS-T 170  
Db 113 paapggplkfsekflftpfslgfefrpgheyyisatppnldvpcrlrkyvyrptnet 172  
QY 171 SHSGEKPVP 180  
Db 173 lyeapepift 182

RESULT 5  
ID AAY06822 standard; Protein; 213 AA.  
XX AAY06822;  
XX 24-JUN-1999 (first entry)  
XX Human LERK-6 polypeptide.  
XX LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury;  
KW cell proliferation; neural growth; neural tissue; neurological disease;  
KW neurodegenerative; excitotoxicity.  
XX Homo sapiens.  
XX WO9910495-A1.  
XX 04-MAR-1999.  
XX 27-AUG-1998; 98WO-US17772.  
XX 29-AUG-1997; 97US-0920440.  
XX (IMMV ) IMMUNEX CORP.  
PI Cerretti DP;  
XX WPI; 1999-243567/20.  
DR N-PSDB; AAX32767.  
XX New cytokine designated LERK-6  
XX Claim 6; Page 42; 46pp; English.  
XX The invention relates murine and human LERK-6 polypeptides that bind to  
CC hek/elk receptors. Host cells transfected or transformed with vectors  
CC comprising the LERK-6 nucleic acid sequences are used for the recombinant  
CC production of the proteins. LERK-6 polypeptides may be useful in the  
CC enhancement, stimulation, proliferation or growth of cells expressing the  
CC hek or elk receptor. The ligand and receptor complex may be involved in  
CC neural growth, development and/or maintenance. LERK-6 can be used for  
CC treating disorders of neural tissue such as injury or neurological  
CC diseases, either chronic or acute. LERK-6 may be employed in treating  
CC neurodegenerative conditions where there is neural death, excitotoxicity.  
CC In addition, they may be administered to a mammal to exert a trophic  
CC effect on neural tissue. They can also be used as reagents for those  
CC conducting quality assurance studies e.g. to monitor shelf life and  
CC stability of elk protein under different conditions. The polypeptides can  
CC also be used as carriers for delivering agents attached to cells bearing  
CC the elk or hek cell surface receptor. The present sequence represents a  
CC human LERK-6 polypeptide.  
XX Sequence 213 AA;

Query Match 33.6%; Score 437; DB 20; Length 213;  
Best Local Similarity 50.5%; Pred. No. 3.7e-36;  
Matches 96; Conservative 24; Mismatches 52; Indels 18; Gaps 7;  
QY 2 AAAPLL-LLLLLVPLPPLLL--AOGPGGALGNRHAVYWNSSNOHLRR-----EGYTVQV 53  
Db 4 adrpilpllllplpppfaraadaarsdryavymrnsprfhagagddggytvev 63  
QY 54 NYNDYLDIYCPHNSGVGPGGAGPGGAEQVLYVMVSRNGYRTCNASQ-GFKRWEKNR 112  
Db 64 sindyldiycphy-----gaplpaermerlylmvngvghascdhrqgrfkrwechr 116  
QY 113 PHAPSPIKFEKFORYSAFSLGYEFHAGHEYYIIS-TPTHNLHWKCLRMKVFVCCAS-T 170  
Db 117 paapggplkfsekflftpfslgfefrpgheyyisatppnavdrpcrlrkyvyrptnet 176  
QY 171 SHSGEKPVP 180  
Db 177 lyeapepift 186

RESULT 6  
ID ABG27837 standard; Protein; 335 AA.  
XX ABG27837;  
XX 18-FEB-2002 (first entry)  
XX Novel human diagnostic protein #27828.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US08631.  
XX 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
XX (HYSE-) HYSEQ INC.  
PI Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS92024.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits and to assess  
CC biodiversity -  
PS Claim 20; SEQ ID No 58196; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations



XX WPI: 1996-188446/19.  
 DR N-PSDB; AAT15009.  
 DR  
 XX Murine and chicken EPH receptor ligand, E1f-1 - useful in diagnosis  
 PPT and treatment of disorders associated with the E1f-1 gene, e.g.  
 PPT dementia, tachycardia, etc.  
 PPT

XX	Claim 1; Page 88-89; 107pp; English.
XX	A novel chicken EPH receptor ligand, Elf-1 (AAR94767), is involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AAR15009) obtd. from an embryo cDNA expression library. This cDNA is used for the prodn. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues and to stimulate or antagonise intracellular signal transduction pathways mediated by the EPH-type receptor.
XX	Sequence 200 AA;
SSQ	Query Match            32.4%; Score 421; DB 17; Length 200; Match Local Similarity 47.5%; Pred. No. 1.4e-34; Matches 86; Conservative 29; Mismatches 50; Indels 16; Gaps 3 AAPLLLLLLLVFPVLPPLLAGPGGALGNRIHAYWNSNQHLREGYTVGVNVNDYDIY 6:        : : :     : : :           : : :     : : :     : : :     : : : 6 aaallaavgcvcv-----wsddpgkvisdryavywnsrnfrhgdytvevsindydiy 6:        : : :     : : :           : : :     : : :     : : :     : : : 63 CPHYNSSVGPGAGPGGGAEPQVLYVMWSRNGYRTCNASQ-GFKRWECNRPAPHAPSPIK 1:      : : :         : : :     : : :     : : :     : : :     : : :     : : : 61 cpध्ये-----plpaermerylyvmnvvegahscdhrgkgfkrwecnrpdpsgplk 1:      : : :         : : :     : : :     : : :     : : :     : : :     : : :

Db	113	fsekqltfrslgrefrgneyyiasppnvdpcikikvyvrtndsl	yespepif	1
QY	180	T	180	
Db	173	t	173	
RESULT	8			
AAW71007				
ID	AAW71007	standard; Protein; 200 AA.		
XX	AAW71007;			
XX	20-OCT-1998	(first entry)		
XX	Amino acid sequence of an avian Elf-1 protein.			
XX	Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP;			
KW	tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation			
KW	intracellular signalling; increased; survival; neuronal cell;			
KW	neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tum			
KW	artificial liver; cartilage; bone formation.			
XX	Gallus sp.			
XX	Key	Location/Qualifiers		
FT	Misc-difference 61..150	/note= "contains a Cys4 motif"		
FT	Misc-difference 35..157	/note= "contains a core sequence motif"		
XX	US5795734-A.			
XX	18-AUG-1998.			
XX	31-MAY-1995;	95US-0455001.		
XX				



```

RESULT 10
AAW02586
ID AAW02586 standard; Protein; 228 AA.
XX
AC AAW02586;
XX
DT 28-NOV-1996 (first entry)
XX
DE Lerk-7 protein.
XX
DE Lerk-6; hek; elk; cell surface receptor; culture; reagent;
KW neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
KW Lerk-7; probe; cytokine.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..20
FT /label= signal_peptide
FT Protein 1..228
FT /label= precursor_protein
FT Domain 1..133
FT /label= extracellular_receptor-binding_domain
FT Region 134..183
FT /label= spacer_region
FT Region 194..208
FT /note= "C-terminal stretch of hydrophobic residues"
FT Binding-site 183
FT /label= GPI_attachment_site
XX
XX W09617925-A1.
PN
XX
XX 13-JUN-1996.
PD
XX
XX 05-DEC-1995; 95WO-US15781.
PF
XX
XX 01-MAR-1995; 95US-0396946.
PR
XX 06-DEC-1994; 94US-0351025.
XX
XX (IMMV ) IMMUNEX CORP.
PA
XX
XX Cerretti DP;
PI
XX
XX WPI; 1996-287171/29.
DR
XX N-PSDB; AAT32699.
DR
XX
XX New isolated human Lerk-7 cytokine - which binds to cell surface
PT receptors elk, hek and eck, useful for delivering agents to cells or
PT for treating neural disorders
PT
XX
XX Claim 1; Page 37-38; 49pp; English.
PS
XX
XX The present sequence is that of human Lerk-7 protein. Lerk-7 is
CC predicted to be anchored to the cell surface via
CC glycosyl-phosphatidylinositol (GPI) linkage. A GPI anchor attaches to the
CC exposed C-terminal amino acid of the processed mature protein, usually
CC after cleavage upstream, often about 10-12 amino acids, of the N-terminus
CC of the hydrophobic domain. Lerk-7 coding sequence (AAT32699) was isolated
CC using a probe derived from the murine Lerk-6 DNA (AAT32700). The Lerk-7
CC gene and protein can be used for studying the role of Lerk-7 in
CC conjunction with elk, hek and eck receptors. They can also be used for
CC delivering diagnostic or therapeutic agents to cells, e.g. cancer cells.
CC The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic
CC properties and can be used to treat neural tissue disorders.
XX
XX Sequence 228 AA;
SQ

Query Match 31.9%; Score 415.5; DB 17; Length 228;
Best Local Similarity 39.5%; Pred. No. 6.1e-34;
Matches 98; Conservative 37; Mismatches 66; Indels 47; Gaps 11;

```

CC damaged or depleted tissues. Antagonists are useful for cancer  
CC treatment. HEK4 BP can also be used to raise antibodies.

XX Sequence 228 AA;

SQ Query Match 31.9%; Score 415.5; DB 17; Length 228;  
Best Local Similarity 39.5%; Pred. No. 6.1e-34;  
Matches 98; Conservative 37; Mismatches 66; Indels 47; Gaps 11;  
Qy 8 LLLLLVPLPLPLAAGPGG-ALGNRHAVYWNSSNOHLRREGTYQVNVNDYLDIYCPHY 66  
Db 6 LLLLLVPLPLPLAAGPGG-ALGNRHAVYWNSSNOHLRREGTYQVNVNDYLDIYCPHY 66  
Qy 67 NSSGYPGAGPGGAGQYVLYMVRNGYRTC-NASQGFKEWECNRPHAPHSPIKFSEK 125  
Db 66 eds-----vpedkterylymvnfygysacdhstsgfkrwecnrphspngplkfsk 117  
Qy 126 FQYSAFSLGYEFHAGHEYYVISTP-THNLHWKCLRMKVFV-----CCASTSHSGEKVPPT 180  
Db 118 fqlftpslgtftrpgreyfysaapdngrscrlkxvfrptnscmktigvhdr----- 173  
Qy 181 LPQFTMGENVKINVLDEPE-----GEN-POVPKLEKISGTSPPKREHLPLAVGI 228  
Db 174 --vfdvndkve-nslepaddtvhesaepsgenaatprij-----psr-----llai 217  
Qy 229 AFFLMTFL 236  
Db 218 llfllaml 225

## RESULT 12

AAW02587  
ID AAW02587 standard; Protein; 184 AA.

XX AAW02587;

XX 28-NOV-1996 (first entry)

XX Lerk-6 protein.

XX Lerk-6; hek; elk; cell surface receptor; culture; reagent;  
XX neuron; disorder; injury; delivery agent; diagnostic; therapeutic;  
XX Lerk-7; probe; cytokine.

XX Mus musculus.

XX WO9617925-A1.

XX 13-JUN-1996.

XX 05-DEC-1995; 95WO-US15781.

XX 01-MAR-1995; 95US-0396946.

XX 06-DEC-1994; 94US-0351025.

XX (IMMV ) IMMUNEX CORP.

XX Cerretti DP;

XX WPI; 1996-287171/29.

XX N-PSDB; AAT32700.

XX New isolated human Lerk-7 cytokine - which binds to cell surface

XX receptors elk, hek and eck, useful for delivering agents to cells or

XX for treating neural disorders

XX Example 1; Page 35; 49pp; English.

XX The present sequence is that of a murine cytokine, Lerk-6, encoded by

XX AAT32700. A fragment of murine Lerk-6 DNA was isolated by PCR for use as

XX a probe for a human Lerk-6 homologue. The probe however led to the

XX identification of a human Lerk-7 gene (see AAT32699). The Lerk-7 gene

CC and protein can be used for studying the role of Lerk-7 in conjunction  
CC with elk, hek and eck receptors. They can also be used for delivering  
CC diagnostic or therapeutic agents to cells, e.g. cancer cells. The  
CC Lerk-7 proteins can also exhibit neuroprotective or neurotrophic  
CC properties and can be used to treat neural tissue disorders.

XX Sequence 184 AA;

SQ Query Match 31.0%; Score 403; DB 17; Length 184;  
Best Local Similarity 50.6%; Pred. No. 8.5e-33;  
Matches 82; Conservative 24; Mismatches 40; Indels 16; Gaps 5;

Qy 28 ALGNRHAYWNSSNOHLRRE-----GYTVQVNVNDYLDIYCPHYNSGSGVGPAGPGG 81

Db 3 anadryavywnsrprfqsvavgdgggytvevsindyldicphy-----gaplpaae 55

Qy 82 GAEQVVLVWSNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFORYSAPSLGYEPHA 140

Db 56 rmeryillymvngvghascdhrqgrfkrwecnrpaagpgplkfsekqiftpslgfeirp 115

Qy 141 GHEYIYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKVPPT 180

Db 116 gheyyisatpnlvdrpclrklkvyrptnetlyeapapift 157

## RESULT 13

AAAR91283

ID AAR91283 standard; Protein; 184 AA.

XX AAR91283;

XX 10-OCT-1996 (first entry)

XX LERK-6 protein.

XX LERK-6; hek; elk; cell surface receptors; culture; reagent;

XX neurons; disorder; injury; delivery agent; diagnostic; therapeutic.

XX Mus musculus.

XX WO9610911-A1.

XX 18-APR-1996.

XX 04-OCT-1995; 95WO-US12779.

XX 03-OCT-1995; 95US-0538709.

XX 05-OCT-1994; 94US-0318393.

XX (IMMV ) IMMUNEX CORP.

XX Cerretti DP;

XX WPI; 1996-209575/21.

XX N-PSDB; AAT14009.

XX Isolated DNA encoding cytokine designated LERK-6 which binds to hek

XX and elk cell surface receptors - useful for drug delivery and

XX screening procedures.

XX Claim 6; Page 34; 44pp; English.

XX The Lerk-6 polypeptide encoded can be used to isolate cells

XX expressing hek/elk cell surface receptors, or to measure the

XX biological activity of such receptors. The protein may also be used

XX as a delivery agent, taking diagnostic and therapeutic agents to

XX cells expressing such receptors. LERK-6 can also be used as a tissue

XX culture reagent to enhance the viability or prolong the lifespan of

XX the neurons. Neural tissue disorders and injuries may be treated by

XX contact with the polypeptide.

XX Sequence 184 AA;

Query Match	31.0%;	Score 403;	DB 20;	Length 184;
Best Local Similarity	50.6%;	Pred. No. 8.5e-33;		
Matches	82;	Conservative	24;	Mismatches 40; Indels 16; Gaps

  

QY	28	ALGNRHAVYWNSSNOHLRRE-----GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPCPGG	81
DB	3	andriyavywnsrnprfqvsavdggytvevsindyldicphy-----gaplppae	55
QY	82	GAEQYVLYMVSRRGYRTCNASQ-GFKRWCNRPAPHSPSIKFKSEKFORYSAFSLGYEFHA	140
DB	56	xmeryilymvggeghascdhrqgfkrcwcnrpaagppklfkseqlfptfsglfeirp	115
QY	141	GHEYIYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVP	180
DB	116	gheyyiyisatpnlvdrcirlkvrvrptnetlyeapepift	157

  

RESULT 15	
AAAR23895	
ID	AAAR23895 standard; Protein; 205 AA.
XX	
AAAR23895:	
XX	
DT	06-NOV-1992 (first entry)
XX	
DE	B61 protein sequence.
XX	
KW	Early inflammatory response; marker; antibody; therapy; induction;
KW	lipopolysaccharides; cytokines; interleukin-2; IL-2; TNF.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	1..18
FT	/note= "signal peptide"
PN	WO9207094-A.
XX	
PD	30-APR-1992.
XX	
PF	15-OCT-1991; 91WO-US07704.
XX	
PR	16-OCT-1990; 90US-0607741.
XX	
PA	(UNMI ) UNIV MICHIGAN.
XX	
PI	Dixit VM;
XX	
DR	WPI; 1992-167172/20.
DR	N-PSDB; AAQ24595.
XX	
PT	Gene prod. used as marker to detect inflammatory response - by
PT	detecting the B61 gene in biological fluids or by using
PT	hybridisation probes
XX	
PS	Claim 7; Fig 3; 39pp; English.
XX	

  

CC	The B1 protein sequence was deduced from the cDNA sequence obt'd. by
CC	screening a cDNA library from human umbilical vein endothelial cells
CC	with radiolabelled cDNA fragments derived from the 5' end of B61 DNA.
CC	The B1 protein has 205 residues (24 kD) comprising a signal
CC	sequence and hydrophobic N- and C- terminal regions. The B61 gene
CC	is involved in early inflammatory response and serves as a marker.
CC	It may be detected by probes or by antibody-based immunoassay of
CC	biological fluids such as plasma, CSF or urine. These assays make
CC	it possible to predict a worsening in a disease process and allow
CC	the quantitative assessment of the magnitude of the inflammatory
CC	response. This information will allow the earlier admin. of
CC	appropriate therapy, thereby shortening the disease process and
CC	limiting the patient's exposure to anti-inflammatory/immuno-
CC	suppressive therapy. B61 induction is rapid and profound, hence



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 27, 2002, 22:50:00 ; Search time 29.18 seconds  
(without alignments)  
199.222 Million cell updates/sec

Title: US-09-904-954-2

Perfect score: 1301

Sequence: 1 MAAAPLLLLLLLLVPVPLPL.....REHLPLAVGIAFFLMTFLAS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

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4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	100.0	238	1	US-08-240-124-2
2	1301	100.0	238	2	US-08-453-943-2
3	1301	100.0	238	2	US-09-057-121-2
4	1301	100.0	238	4	US-09-358-734-2
5	1261	96.9	234	1	US-08-299-567-5
6	437	33.6	209	1	US-08-455-001-2
7	437	33.6	209	1	US-08-308-814-2
8	437	33.6	209	5	PCT-US95-11869-2
9	437	33.6	213	1	US-09-609-324A-10
10	437	33.6	213	2	US-08-920-440B-10
11	437	33.6	213	4	US-09-173-492-10
12	437	33.6	213	4	US-09-173-133-10
13	421	32.4	200	1	US-08-455-001-4
14	421	32.4	200	5	PCT-US95-11869-4
15	415.5	31.9	228	1	US-08-442-248-4
16	415.5	31.9	228	1	US-08-440-815-4
17	415.5	31.9	228	3	US-08-379-802-2
18	415.5	31.9	228	3	US-09-048-129-2
19	415.5	31.9	228	4	US-09-048-079-2
20	415.5	31.9	228	4	US-08-486-449-4
21	415.5	31.9	228	5	PCT-US95-15781-5
22	403	31.0	184	1	US-09-609-324A-2
23	403	31.0	184	2	US-08-920-440B-2
24	403	31.0	184	4	US-09-173-492-2
25	403	31.0	184	4	US-09-173-133-2
26	403	31.0	184	4	US-09-165-533-2
27	403	31.0	184	5	PCT-US95-12779-2

28 403 31.0 184 5 PCT-US95-15781-2 Sequence 2, Appli  
29 390 30.0 205 1 US-08-321-162-2 Sequence 2, Appli  
30 390 30.0 205 1 US-08-448-736-1 Sequence 1, Appli  
31 390 30.0 205 1 US-08-441-216-2 Sequence 2, Appli  
32 390 30.0 205 1 US-08-452-779-1 Sequence 1, Appli  
33 390 30.0 205 1 US-08-299-567-4 Sequence 4, Appli  
34 390 30.0 205 2 US-08-445-065-1 Sequence 12, Appli  
35 390 30.0 205 2 US-08-445-065-12 Sequence 1, Appli  
36 390 30.0 205 3 US-08-959-524-1 Sequence 12, Appli  
37 390 30.0 205 3 US-08-959-524-12 Sequence 5, Appli  
38 364.5 28.0 179 1 US-08-455-001-5 Sequence 5, Appli  
39 364.5 28.0 179 5 PCT-US95-11869-5 Sequence 4, Appli  
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41 364.5 28.0 201 1 US-08-453-943-4 Sequence 4, Appli  
42 364.5 28.0 201 2 US-09-057-121-4 Sequence 4, Appli  
43 364.5 28.0 201 4 US-09-358-734-4 Sequence 8, Appli  
44 334 25.7 104 1 US-09-609-324A-8 Sequence 8, Appli  
45 334 25.7 104 2 US-08-920-440B-8 Sequence 8, Appli

## ALIGNMENTS

RESULT 1  
US-08-240-124-2  
; Sequence 2, Application US/08240124  
; Patent No. 5516658  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEX  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240,124  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 238 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-240-124-2

Query Match 100.0%; Score 1301; DB 1; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.7e-128;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAAPLLLLLLVPPVPLPPLLAQGGGALGNHRHAYVWSSNOHLRREGTYVQVNVNDYLD 60  
|||||  
Db 1 MAAAPLLLLLLVPPVPLPPLLAQGGGALGNHRHAYVWSSNOHLRREGTYVQVNVNDYLD 60  
|||||

Qy 61 IYCPHNSGVGPGAGPGGAGQVLYVMVSRNGYRTCNASQGFKECNRPHAPHSPI 120  
|||||  
Db 61 IYCPHNSGVGPGAGPGGAGQVLYVMVSRNGYRTCNASQGFKECNRPHAPHSPI 120  
|||||

Qy 121 KFSEKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFYCCASTSHSGEKPVP 180  
|||||  
Db 121 KFSEKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFYCCASTSHSGEKPVP 180  
|||||

Qy 181 LPQFTMGPNVKINVLDEFEENPQVPKLEKSIKSGTSPKREHLPLAVGIAFFLMTFLAS 238  
|||||  
Db 181 LPQFTMGPNVKINVLDEFEENPQVPKLEKSIKSGTSPKREHLPLAVGIAFFLMTFLAS 238  
|||||

RESULT 2  
US-08-453-943-2  
; Sequence 2, Application US/08453943  
; Patent No. 5738844  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/453.943  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/240,124  
; FILING DATE: 09-MAY-1994  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 238 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-453-943-2

Query Match 100.0%; Score 1301; DB 1; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.7e-128;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAAAPLLLLLLVPPVPLPPLLAQGGGALGNHRHAYVWSSNOHLRREGTYVQVNVNDYLD 60  
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Qy 61 IYCPHNSGVGPGAGPGGAGQVLYVMVSRNGYRTCNASQGFKECNRPHAPHSPI 120  
|||||  
Db 61 IYCPHNSGVGPGAGPGGAGQVLYVMVSRNGYRTCNASQGFKECNRPHAPHSPI 120  
|||||

Qy 121 KFSEKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFYCCASTSHSGEKPVP 180  
|||||  
Db 121 KFSEKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFYCCASTSHSGEKPVP 180  
|||||

Qy 181 LPQFTMGPNVKINVLDEFEENPQVPKLEKSIKSGTSPKREHLPLAVGIAFFLMTFLAS 238  
|||||  
Db 181 LPQFTMGPNVKINVLDEFEENPQVPKLEKSIKSGTSPKREHLPLAVGIAFFLMTFLAS 238  
|||||

RESULT 3  
US-08-453-943-2  
; Sequence 2, Application US/09057121  
; Patent No. 5969110  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,121  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/240,124  
; FILING DATE:  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 238 amino acids



; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-057-121-2

Query Match 100.0%; Score 1301; DB 2; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.7e-128;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPLLLLLLVPVPLLLPGLAOGPGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
DB 1 MAAPLLLLLLVPVPLLLPGLAOGPGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
QY 61 IYCPHYNSSGVGPGAGPGGGAQEQVLYVMVSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
DB 61 IYCPHYNSSGVGPGAGPGGGAQEQVLYVMVSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
QY 121 KFSEKFORYSAFSLGYEFHAGHEYYYISTPTNHLHWKCLRMKVFVCCASTSHSGEKPVT 180  
DB 121 KFSEKFORYSAFSLGYEFHAGHEYYYISTPTNHLHWKCLRMKVFVCCASTSHSGEKPVT 180  
QY 181 LPQFTMGPNVKINVLDFEGENQVPKLEKSISGTSKPREHLPVAGIAFFLMTFLAS 238  
DB 181 LPQFTMGPNVKINVLDFEGENQVPKLEKSISGTSKPREHLPVAGIAFFLMTFLAS 238

## RESULT 4

US-09-358-734-2  
; Sequence 2, Application US/09358734  
; Patent No. 6274117  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/358,734  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/240,124  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 238 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-358-734-2

Query Match 100.0%; Score 1301; DB 4; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.7e-128;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPLLLLLLVPVPLLLPGLAOGPGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
DB 1 MAAPLLLLLLVPVPLLLPGLAOGPGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
QY 61 IYCPHYNSSGVGPGAGPGGGAQEQVLYVMVSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
DB 61 IYCPHYNSSGVGPGAGPGGGAQEQVLYVMVSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
QY 121 KFSEKFORYSAFSLGYEFHAGHEYYYISTPTNHLHWKCLRMKVFVCCASTSHSGEKPVT 180  
DB 121 KFSEKFORYSAFSLGYEFHAGHEYYYISTPTNHLHWKCLRMKVFVCCASTSHSGEKPVT 180  
QY 181 LPQFTMGPNVKINVLDFEGENQVPKLEKSISGTSKPREHLPVAGIAFFLMTFLAS 238  
DB 181 LPQFTMGPNVKINVLDFEGENQVPKLEKSISGTSKPREHLPVAGIAFFLMTFLAS 238

## RESULT 5

US-08-299-567-5  
; Sequence 5, Application US/08299567  
; Patent No. 5747033  
; GENERAL INFORMATION:  
; APPLICANT: Davis, et al.  
; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL  
; TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
; STREET: 777 Old Saw Mill River Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-6707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,567  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kempier, Gail M.  
; REGISTRATION NUMBER: 32,143  
; REFERENCE/DOCKET NUMBER: REG 290  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 914-345-7400  
; TELEFAX: 914-345-7721  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-08-299-567-5

Query Match 96.9%; Score 1261; DB 1; Length 234;  
Best Local Similarity 97.9%; Pred. No. 4e-124;  
Matches 233; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 MAAPLPLLLLVPPVPLPPLLAQGGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
DB 1 MAAPLPLLLLVPPVPLPPLLAQGGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
QY 61 IYCPHNSGVGPGAGPGGGAGQVLYMYVSRNGYRTCNASQGFKRWECPHAPHSP1 120  
DB 61 IYCPHNSG----GAGPGGGAGQVLYMYVSRNGYRTCNASQGFKRWECPHAPHSP1 116  
QY 121 KFSEKQRYSAFSLGYEFHAGHEYYIISTPTNHLHWKCLRMKVFVCCASTSHSGKPVPT 180  
DB 117 KFSEKQRYSAFSLGYEFHAGHEYYIISTPTNHLHWKCLRMKVFVCCASTSHSGKPVPT 176  
QY 181 LPQFTMGPNVKINVLDEGENQVPKLEKISGTSKREHPLAVGIAFFLMTFLAS 238  
DB 177 LPQFTMGPNVKINVLDEGENQVPKLEKISGTSKREHPLAVGIAFFLMTFLAS 234

RESULT 6

US-08-455-001-2  
; Sequence 2, Application US/08455001  
; Patent No. 5795734  
; GENERAL INFORMATION:  
; APPLICANT: Flanagan, John G.  
; APPLICANT: Cheng, Hwai-Jong  
; TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related  
; TITLE OF INVENTION: Thereto  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,001  
; FILING DATE: 31 MAY 1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: HMI-011CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 209 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-455-001-2

Query Match 33.6%; Score 437; DB 1; Length 209;  
Best Local Similarity 50.5%; Pred. No. 5.4e-38;  
Matches 96; Conservative 25; Mismatches 47; Indels 22; Gaps 7;

QY 2 AAAPLPLLLLVPPVPLPPLLA--QGPGGALGNRHAVYWNSSNOHLRRE-----GYTVQV 53  
DB 4 AORPLPLPLLL-----LLPLARNEDPARANADRVAVYWNRSNPRFQVSAVGDDGGYTV 59  
QY 54 NVNDYLDIYCPHYNSGVGPGGAGQVLYMYVSRNGYRTCNASQ--GFKRWECPH 112  
DB 60 SINDYLDIYCPHY-----GAPLPAPARMERYILYMYVNGEGHASCDSHRQGRKWECPH 112  
QY 113 PHAPHSPIKFSEKQRYSAFSLGYEFHAGHEYYIIS--TPTNHLHWKCLRMKVFVCCAS-T 170  
DB 113 PHAPHSPIKFSEKQRYSAFSLGYEFHAGHEYYIIS--TPTNHLHWKCLRMKVFVCCAS-T 170

..

DB 113 PAAPGGPLKFSEKQRYSAFSLGYEFHAGHEYYIISATPPNLVDRPCLRLKVVYVRPTNET 172  
QY 171 SHSGKPVPT 180  
DB 173 LYEAPEPIFT 182  
RESULT 7  
US-08-308-814-2  
; Sequence 2, Application US/08308814  
; Patent No. 6268476  
; GENERAL INFORMATION:  
; APPLICANT: Flanagan, John G.  
; APPLICANT: Cheng, Hwai-Jong  
; TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related  
; TITLE OF INVENTION: Thereto  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/308,814  
; FILING DATE: 19-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: HMI-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 209 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-308-814-2

Query Match 33.6%; Score 437; DB 4; Length 209;  
Best Local Similarity 50.5%; Pred. No. 5.4e-38;  
Matches 96; Conservative 25; Mismatches 47; Indels 22; Gaps 7;

QY 2 AAAPLPLLLLVPPVPLPPLLA--QGPGGALGNRHAVYWNSSNOHLRRE-----GYTVQV 53  
DB 4 AORPLPLPLLL-----LLPLARNEDPARANADRVAVYWNRSNPRFQVSAVGDDGGYTV 59  
QY 54 NVNDYLDIYCPHYNSGVGPGGAGQVLYMYVSRNGYRTCNASQ--GFKRWECPH 112  
DB 60 SINDYLDIYCPHY-----GAPLPAPARMERYILYMYVNGEGHASCDSHRQGRKWECPH 112  
QY 113 PHAPHSPIKFSEKQRYSAFSLGYEFHAGHEYYIIS--TPTNHLHWKCLRMKVFVCCAS-T 170  
DB 113 PHAPHSPIKFSEKQRYSAFSLGYEFHAGHEYYIIS--TPTNHLHWKCLRMKVFVCCAS-T 170  
QY 171 SHSGKPVPT 180  
DB 173 LYEAPEPIFT 182

RESULT 8  
PCT-US95-11869-2  
; Sequence 2, Application PC/TUS9511869

GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: BPH Receptor Ligands, and Uses Related  
TITLE OF INVENTION: Theteto  
NUMBER OF SEQUENCES: 5  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/11869  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: HMI-011CPCP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 209 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-11869-2

Query Match 33.6%; Score 437; DB 5; Length 209;  
Best Local Similarity 50.5%; Pred. No. 5.4e-38;  
Matches 96; Conservative 25; Mismatches 47; Indels 22; Gaps 7;  
QY 2 AAAPLLLLLVVPLPLLA--OGPGGALGNHNAVYWNSSNQHLR-----GYTVQV 53  
Db 4 AQRPLLLLLLVVPLPLLA--OGPGGALGNHNAVYWNSSNQHLR-----GYTVQV 59  
QY 54 NVNDYLDIYCPHYNSGPGGAGPGGAEQVYLYVMVSRNGYRTCNASQ--GFKRWECNR 112  
Db 60 SINDYLDIYCPHY-----GAPLPPAERMEHYLYVMVNGEGHASCDDHQRGFRWECNR 112  
QY 113 PHAPSPKSEKQRYSAFSLGFEHAGHEYYIIS--TPTHNLHWKCLRMKVFVCCAS-T 170  
Db 113 PAAPGGPLKFESEKQRYSAFSLGFEHAGHEYYIIS--TPTHNLHWKCLRMKVFVCCAS-T 172  
QY 171 SHSGEKPVT 180  
Db 173 LYEAPDIFT 182

RESULT 9  
US-09-324A-10  
Sequence 10, Application US/09609324A  
Patent No. RE37582  
GENERAL INFORMATION:  
APPLICANT: CERRETTI, Douglas P.  
TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6  
FILE REFERENCE: A7772  
CURRENT APPLICATION NUMBER: US/09/609,324A  
CURRENT FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 08/920,440  
PRIOR FILING DATE: 1997-08-29  
PRIOR APPLICATION NUMBER: 08/538,709  
PRIOR FILING DATE: 1995-10-03  
PRIOR APPLICATION NUMBER: 08/318,393  
PRIOR FILING DATE: 1994-10-05  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 10  
LENGTH: 213  
TYPE: PRT  
ORGANISM: LERK-6  
US-09-609-324A-10

Query Match 33.6%; Score 437; DB 1; Length 213;  
Best Local Similarity 50.5%; Pred. No. 5.6e-38;  
Matches 96; Conservative 24; Mismatches 52; Indels 18; Gaps 7;  
QY 2 AAAPLL--LLLLVPVPLPL--AQPGGALGNHNAVYWNSSNQHLR-----EGYTVQV 53  
Db 4 AQRPLLLLLLVVPLPL--AQPGGALGNHNAVYWNSSNQHLR-----EGYTVQV 63  
QY 54 NVNDYLDIYCPHYNSGPGGAGPGGAEQVYLYVMVSRNGYRTCNASQ--GFKRWECNR 112  
Db 64 SINDYLDIYCPHY-----GAPLPPAERMEHYLYVMVNGEGHASCDDHQRGFRWECNR 116  
QY 113 PHAPSPKSEKQRYSAFSLGFEHAGHEYYIIS--TPTHNLHWKCLRMKVFVCCAS-T 170  
Db 117 PAAPGGPLKFESEKQRYSAFSLGFEHAGHEYYIIS--TPTHNLHWKCLRMKVFVCCAS-T 176  
QY 171 SHSGEKPVT 180  
Db 177 LYEAPDIFT 186

RESULT 10  
US-08-920-440B-10  
Sequence 10, Application US/08920440B  
Patent No. 5919905  
GENERAL INFORMATION:  
APPLICANT: Cerretti, Douglas P.  
TITLE OF INVENTION: Cytokine Designated LERK-6  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: System 7.6  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/920,440B  
FILING DATE: 29-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C.  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2826-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-920-440B-10

Query Match 33.6%; Score 437; DB 2; Length 213;  
Best Local Similarity 50.5%; Pred. No. 5.6e-38;  
Matches 96; Conservative 24; Mismatches 52; Indels 18; Gaps 7;  
QY 2 AAAPLL--LLLLVPVPLPL--AQPGGALGNHNAVYWNSSNQHLR-----EGYTVQV 53  
Db 4 AQRPLLLLLLVVPLPL--AQPGGALGNHNAVYWNSSNQHLR-----EGYTVQV 63  
QY 54 NVNDYLDIYCPHYNSGPGGAGPGGAEQVYLYVMVSRNGYRTCNASQ--GFKRWECNR 112

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RESULT 12
US-09-173-133-10
; Sequence 10, Application US/09173133
; Patent No. 623247
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; TITLE OF INVENTION: Cytokine Designated LERK-6
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: System 7.6
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/173,133
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,440
; FILING DATE: 29-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2826-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-173-133-10

Query Match          33.6%; Score 437; DB 4; Length 213;
Best Local Similarity 50.5%; Pred. No. 5,6e-38;
Matches 96; Conservative 24; Mismatches 52; Indels 18; Gaps

QY   2 AAAPLL-LLLLLVPVPLPLL-AAQGPGGALGNRHAVYNWSSNOHLRR-----EGYTVOV 53
      ||| |||||:||: | : | : ||||| || |||||:|
Db   4 AQPELLLLLLLLLPLPPPFARAEDAARANSRDYAYWNRSNPRFHAGAGDDGGGYTVEV 63
      ||| |||||:||: | : | : ||||| || |||||:|

QY   54 NVNDYLDIYCYPHNSSGVGFGAGPGGGAEQVYLVMVRNGRYRTCNASQ-GFKRWECLR 112
      ::|||||||::| | |||||: | : |: | |||||
Db   64 SINDYLDIYCPHY-----GAPLPAERMHEHYLVYWNGEGHASCDHRQRGFKRWECLR 116
      ::|||||||::| | |||||: | : |: | |||||

QY   113 PHAPHSPIKESEKFQSYAFSLGYEFHAGEHYIIIS-TPTHNLHWKCLRMKVVCAS-T 170
      | || :||||||| :: |||||:| ||||| || : | : |||||:| : |
Db   117 PAAPGPGLPKFEKSFQLFTPFLSGFERPGHEYIIISATPPNAVDRPCLRKLKYVVRTNET 176
      || : ||: | : ||: | : ||: | : ||: | : ||: | : ||: | : ||: |

QY   171 SHSGEKPVPT 180
      : : | : |
Db   177 LYEAPEPIFT 186
```

```

; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMI-011CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-11869-4

Query Match          32.4%; Score 421; DB 5; Length 200;
Best Local Similarity 47.5%; Pred. No. 2,4e-36;
Matches 86; Conservative 29; Mismatches 50; Indels 16; Gaps 5;

QY 3 AAPLLLLLVVPLPLLAQGGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLDIY 62
   ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 6 AAALLAAIVGCV-----WSDPGKVISDRYAVYWNRSNPRFHRGDTVVEVSINDYLDIY 60

QY 63 CPHYNSSGVGGAGPGGGAGAEQVLLVWVSRNGYFTCNASQ-GFKRWECNRPAPHSPIK 121
   ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 61 CPHYEE-----PLPAERMERVLLVWVNYEGHASCDSHQKGFGRWECNRPDPSGPLK 112

QY 122 FSKFKORYSALGYPEFHAGHEYIIS-TPTHNLRLWRKLRMKVTVCCASTS-HSGEKPPV 179
   ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 113 FSEKQFLTFPSLGFERPGHEYIISASPNVVDRLCLKLVIVRPTNDSLSPPEPIF 172

QY 180 T 180
Db 173 T 173

```

RESULT 15  
US-08-442-248--4  
; Sequence 4, Application US/08442248  
; Patent No. 5759863  
; GENERAL INFORMATION:  
; APPLICANT: Caras, Ingrid W.  
; APPLICANT: Winslow, John W.  
; TITLE OF INVENTION: AL-1 Neurotrophic Factor  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,248  
; FILING DATE: 15-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/330128  
; FILING DATE: 27-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: 920C4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-8674  
; TELEFAX: 415/952-9861  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-442-248-4

Query Match	31.98;	Score 415.5;	DB 1;	Length 228;
Best Local Similarity	39.5%;	Pred. No. 1.1e-35;		
Matches	98;	Conservative 37;	Mismatches 66;	Indels 47; Gaps 11;

  

Qy	8	LLLLVPPVPLPLLAQGGG--ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY	66
Db	6	MLTLVFLVMCVFSQDPGSAVDRAVYWNSSNPRFORGDYHIDVCINDYLDVFCPHY	65
Qy	67	NSSGVGPGAGPGGGAQYVLYMVRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK	125
Db	66	EDS-----VPEDKTERVLYVMVDFDGYSGACDHTSKGFKRWECNRPHSPNGPLKFSEK	117
Qy	126	FORYSAFSLGYEFHAGHEYIYSTP--THNLHWKCLRMKVYV-----CCASTSHSGEKPVP	180
Db	118	FQLETPESLGFEPFGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDR----	173
Qy	181	LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI	228
Db	174	--VFDVNDKVB--NSLEPADTVHESAEPSSRGNAATPRI-----PSR-----LLAI	217
Qy	229	AFFLMTFL	236
Db	218	LLFLAML	225

Search completed: September 28, 2002, 01:37:42
Job time: 10062 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 28, 2002, 01:28:35 ; Search time 251.33 Seconds  
(without alignments)  
333.312 Million cell updates/sec

Title: US-09-904-954-2

Perfect score: 1301

Sequence: 1 MAAAPLLLLLLVPVPLPL.....REHLPLAVGIAFFLMTFLAS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:

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- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pcp.\*
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- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pcp.\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pcp.\*
- 21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pcp.\*
- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pcp.\*
- 23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pcp.\*
- 24: /cgn2\_6/ptodata/2/paa/US100\_COMB.pcp.\*
- 25: /cgn2\_6/ptodata/2/paa/US101\_COMB.pcp.\*
- 26: /cgn2\_6/ptodata/2/paa/US102\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	100.0	238	1	PCT-US94-09282-2
2	1301	100.0	238	5	US-08-109-745-2
3	1301	100.0	238	5	US-08-161-132-2
4	1301	100.0	238	21	US-09-733-756-2
5	1301	100.0	238	23	US-09-904-954-2
6	1301	100.0	238	23	US-09-948-941-315
7	1301	100.0	238	23	US-09-948-941-360

8	1285.5	98.8	237	11	US-08-730-700A-16	Sequence 16, Appl
9	1285.5	98.8	237	20	US-09-621-595-16	Sequence 16, Appl
10	1266	97.3	234	6	US-08-329-402-7	Sequence 7, Appli
11	1261	96.9	234	7	US-08-327-423-5	Sequence 5, Appli
12	1250.5	96.1	233	11	US-08-730-700A-15	Sequence 15, Appl
13	1250.5	96.1	233	20	US-09-621-595-15	Sequence 15, Appl
14	1227.5	94.4	233	16	US-09-214-631-7	Sequence 335, App
15	776	56.8	776	26	US-60-212-656-335	Sequence 562, App
16	481	37.0	91	26	US-60-207-216-562	Sequence 6, Appli
17	444.5	34.2	93	6	US-08-222-075-6	Sequence 6, Appli
18	444.5	34.2	93	6	US-08-229-402-6	Sequence 2, Appli
19	437	33.6	209	7	US-08-393-462-2	Sequence 2, Appli
20	437	33.6	209	15	US-09-135-129-2	Sequence 2, Appli
21	437	33.6	209	23	US-09-921-984-2	Sequence 10, Appl
22	437	33.6	213	19	US-09-580-236A-10	Sequence 6, Appli
23	435	33.4	209	16	US-09-214-631-6	Sequence 6, Appli
24	426.5	32.8	335	1	PCT-US01-08631-58196	Sequence 14, Appl
25	421.5	32.4	208	11	US-08-730-700A-14	Sequence 14, Appl
26	421.5	32.4	208	20	US-09-621-595-14	Sequence 4, Appli
27	421	32.4	200	7	US-08-393-462-4	Sequence 4, Appli
28	421	32.4	200	15	US-09-135-129-4	Sequence 4, Appli
29	415.5	31.9	228	7	US-08-330-128-4	Sequence 5, Appli
30	415.5	31.9	228	7	US-08-396-946-5	Sequence 4, Appli
31	415.5	31.9	228	8	US-08-440-567-4	Sequence 4, Appli
32	415.5	31.9	228	8	US-08-442-249-4	Sequence 4, Appli
33	415.5	31.9	228	9	US-08-578-684-4	Sequence 4, Appli
34	415.5	31.9	228	11	US-08-766-239-4	Sequence 4, Appli
35	415.5	31.9	228	12	US-08-832-660-5	Sequence 2, Appli
36	415.5	31.9	228	19	US-09-570-327-2	Sequence 2, Appli
37	415.5	31.8	228	16	US-09-214-631-9	Sequence 2, Appli
38	413.5	31.0	184	7	US-08-318-393A-2	Sequence 2, Appli
39	403	31.0	184	9	US-08-396-946-2	Sequence 2, Appli
40	403	31.0	184	9	US-08-538-709-2	Sequence 2, Appli
41	403	31.0	184	12	US-08-832-660-2	Sequence 2, Appli
42	403	31.0	184	15	US-09-165-861-2	Sequence 2, Appli
43	403	31.0	184	19	US-09-580-236A-2	Sequence 2, Appli
44	401.5	30.9	92	18	US-09-474-434-1651	Sequence 1651, Ap

ALIGNMENTS

RESULT 1  
PCT-US94-09282-2  
Sequence 2, Application PC/TUS9409282  
GENERAL INFORMATION:  
APPLICANT: BECKMANN, M. P.  
APPLICANT: CERRETTI, DOUGLAS P.  
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
TITLE OF INVENTION: RECEPTOR HEX  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple System 7.1  
SOFTWARE: Microsoft Word for Apple, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09282  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,132  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/114,426

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; FILING DATE: 30-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/109,745
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SEESE, KATHRYN A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2814-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-09282-2

Query Match 100.0%; Score 1301; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.5e-123;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAPLLLLLLVPVPLPPLLAQGGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60
Db 1 MAAPLLLLLLVPVPLPPLLAQGGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60
Qy 61 IYCPHYNSSGVGPGAGPGGGAEQYVLYMYSRNGYRTCNASQGFKRWCENRPHAPHSPI 120
Db 61 IYCPHYNSSGVGPGAGPGGGAEQYVLYMYSRNGYRTCNASQGFKRWCENRPHAPHSPI 120
Qy 121 KFSEKFORYSAFSLGYESFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKVPPT 180
Db 121 KFSEKFORYSAFSLGYESFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKVPPT 180
Qy 181 LPQFTMGPNVKINVLDFEGENPQVPKLEKISGTSFKREHLPLAVGIAFFLMTFLAS 238
Db 181 LPQFTMGPNVKINVLDFEGENPQVPKLEKISGTSFKREHLPLAVGIAFFLMTFLAS 238

RESULT 2
US-08-109-745-2
; Sequence 2, Application US/08109745
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; TITLE OF INVENTION: RECEPTOR HEK
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/109,745
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SEESE, KATHRYN A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2814
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
```

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; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-109-745-2

Query Match 100.0%; Score 1301; DB 5; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.5e-123;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAPLLLLLLVPVPLPPLLAQGGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60
Db 1 MAAPLLLLLLVPVPLPPLLAQGGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60
Qy 61 IYCPHYNSSGVGPGAGPGGGAEQYVLYMYSRNGYRTCNASQGFKRWCENRPHAPHSPI 120
Db 61 IYCPHYNSSGVGPGAGPGGGAEQYVLYMYSRNGYRTCNASQGFKRWCENRPHAPHSPI 120
Qy 121 KFSEKFORYSAFSLGYESFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKVPPT 180
Db 121 KFSEKFORYSAFSLGYESFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKVPPT 180
Qy 181 LPQFTMGPNVKINVLDFEGENPQVPKLEKISGTSFKREHLPLAVGIAFFLMTFLAS 238
Db 181 LPQFTMGPNVKINVLDFEGENPQVPKLEKISGTSFKREHLPLAVGIAFFLMTFLAS 238

RESULT 3
US-08-161-132-2
; Sequence 2, Application US/08161132
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; TITLE OF INVENTION: RECEPTOR HEK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/161,132
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/114,426
; FILING DATE: 30-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/109,745
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SEESE, KATHRYN A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2814-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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Qy	1	MAAPLPIIIIIIIIVPVPILP	LLAAGPGGALGNRIHAYV	WNSNOHLRREGYTVQVNVNDYLD	60
Db	1	MAAAPLPIIIIIIIIVPVPILP	LLAAGPGGALGNRIHAYV	WNSNOHLRREGYTVQVNVNDYLD	60
Qy	61	IYCHYNSSGVGPCAGPGGGGAEQYVLY	VMVSRNGYPTCNASOGFKRWCNRRPHAPHSPI	120	
Db	61	IYCHYNSSGVGPCAGPGGGGAEQYVLY	VMVSRNGYPTCNASOGFKRWCNRRPHAPHSPI	120	
Qy	121	KFSEKFORYSAFSLGYEFHAGHEYIYSTPT	HNHLHWKLRMKVFVCCASTSHSGEKPVPPT	180	
Db	121	KFSEKFORYSAFSLGYEFHAGHEYIYSTPT	HNHLHWKLRMKVFVCCASTSHSGEKPVPPT	180	

1	60
2	60
3	120
4	120
5	180
6	180

Qy	1	MAAAPLLLLLLVPVPLPLPPLLAQPGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD	60
Db	1	MAAAPLLLLLLVPVPLPLPPLLAQPGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD	60
Qy	61	IYCPHYNSSGVPCAGPGCGGAEQVLYWVSNRGYRTCNASOGFKRWECPNPHAPHSP	120
Db	61	IYCPHYNSSGVPCAGPGCGGAEQVLYWVSNRGYRTCNASOGFKRWECPNPHAPHSP	120
Qy	121	KFSEKFORYSFSLGYEFHAGHEYYYISTPTNLHWKCLRMKFVYCCASTSHSGEKPVPT	180
Db	121	KFSEKFORYSFSLGYEFHAGHEYYYISTPTNLHWKCLRMKFVYCCASTSHSGEKPVPT	180
Qy	181	LPQTMGPNNKINVLDFEGENFQVPKLEKISGTSPPKREHPLAVGIAFFLMTFLAS	238

Db 181 LPQFTMGPNVKINVLEDFEGENPOVPVKLEKISGTSKREHLPLAVGIAFFLMTFLAS 238  
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RESULT 6  
US-09-948-941-315  
; Sequence 315, Application US/09948941  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH CANCER, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL000788  
; CURRENT APPLICATION NUMBER: US/09/948,941  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,328  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 12618  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 315  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Human  
US-09-948-941-315

Query Match 100.0%; Score 1301; DB 23; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.5e-123;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MAAAPLLLLLLLLLVPPVPLPPLLAQPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60  
|||||  
Qy 61 IYCPHYNSGVPAGPGAGPGGAEQVLYMYSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
|||||  
Db 61 IYCPHYNSGVPAGPGAGPGGAEQVLYMYSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
|||||  
Qy 121 KFSEKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKPVP 180  
|||||  
Db 121 KFSEKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKPVP 180  
|||||  
Qy 181 LPQFTMGPNVKINVLEDFEGENPOVPVKLEKISGTSKREHLPLAVGIAFFLMTFLAS 238  
|||||  
Db 181 LPQFTMGPNVKINVLEDFEGENPOVPVKLEKISGTSKREHLPLAVGIAFFLMTFLAS 238  
|||||

RESULT 7  
US-09-948-941-360  
; Sequence 360, Application US/09948941  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH CANCER, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL000788  
; CURRENT APPLICATION NUMBER: US/09/948,941  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR FILING DATE:  
; PRIOR APPLICATION NUMBER: 60/231,328  
; NUMBER OF SEQ ID NOS: 12618  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 360  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Human  
US-09-948-941-360

Query Match 100.0%; Score 1301; DB 23; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.5e-123;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAAAPLLLLLLLLLVPPVPLPPLLAQPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60  
|||||

Db 1 MAAAPLLLLLLLLLVPPVPLPPLLAQPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60  
|||||  
Qy 61 IYCPHYNSGVPAGPGAGPGGAEQVLYMYSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
|||||  
Db 61 IYCPHYNSGVPAGPGAGPGGAEQVLYMYSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
|||||  
Qy 121 KFSEKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKPVP 180  
|||||  
Db 121 KFSEKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKPVP 180  
|||||  
Qy 181 LPQFTMGPNVKINVLEDFEGENPOVPVKLEKISGTSKREHLPLAVGIAFFLMTFLAS 238  
|||||  
Db 181 LPQFTMGPNVKINVLEDFEGENPOVPVKLEKISGTSKREHLPLAVGIAFFLMTFLAS 238  
|||||

## RESULT 8

US-08-730-700A-16  
; Sequence 16, Application US/08730700A  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; APPLICANT: Henkemeyer, Mark  
; TITLE OF INVENTION: Method of Activating a Novel Ligand  
; TITLE OF INVENTION: Regulatory Pathway  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Room 970  
; STREET: 600 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1X5  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/730,700A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/005,518  
; FILING DATE: 13-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurtydyk, Linda M.  
; REGISTRATION NUMBER: 34,971  
; REFERENCE/DOCKET NUMBER: 3153-196  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 416-586-3235  
; TELEFAX: 416-586-3110  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 237 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-730-700A-16

Query Match 98.8%; Score 1285.5; DB 11; Length 237;  
Best Local Similarity 99.6%; Pred. No. 9.3e-122;  
Matches 237; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MAAAPLLLLLLLLLVPPVPLPPLLAQPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60  
|||||  
Db 1 MAAAPLLLLLLLLLVPPVPLPPLLAQPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60  
|||||  
Qy 61 IYCPHYNSGVPAGPGAGPGGAEQVLYMYSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
|||||  
Db 61 IYCPHYNSGVPAGPGAGPGGAEQVLYMYSRNGYRTCNASQGFKRWEKNRPHAPHSPI 120  
|||||  
Qy 121 KFSEKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKPVP 180  
|||||

Db 121 KFSEKF-RYSAFSLGYEFHAGHEYYISTPTNHLHWKLRMKVFCVCCASTSHSGEKPVT 179  
Qy 181 LPQFTMGPNVKINLVLEDFEGENPOVPKLEKSIGTSPKREHLPLAVGIAFFLMTFLAS 238  
Db 180 LPQFTMGPNVKINLVLEDFEGENPOVPKLEKSIGTSPKREHLPLAVGIAFFLMTFLAS 237

RESULT 9  
US-09-621-595-16  
; Sequence 16, Application US/09621595  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; TITLE OF INVENTION: Method of Activating a Novel Ligand  
; REGULATORY PATHWAY  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Room 970  
; STREET: 600 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1X5  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/621,595  
; FILING DATE: 21-Jul-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/730,700  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurdydyk, Linda M.  
; REGISTRATION NUMBER: 34,971  
; REFERENCE/DOCKET NUMBER: 3153-196  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 416-586-3235  
; TELEFAX: 416-586-3110  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 237 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-621-595-16

Query Match 98.8%; Score 1285.5; DB 20; Length 237;  
Best Local Similarity 99.8%; Pred. No. 9.3e-122;  
Matches 237; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MAAAPLLLLLVLPVPLPLLAQPGGALGNHRHAYVWNSNOHLRREGYTVQVNVNDYLD 60  
Db 1 MAAAPLLLLLVLPVPLPLLAQPGGALGNHRHAYVWNSNOHLRREGYTVQVNVNDYLD 60

Qy 61 IYCPHYNSSGVGPGAGPGGAEQYVLYMYVRNGYRTCNASQGFKRWECPHAPHSP 120  
Db 61 IYCPHYNSSGVGPGAGPGGAEQYVLYMYVRNGYRTCNASQGFKRWECPHAPHSP 120

Qy 121 KFSEKFORYSAFSLGYEFHAGHEYYISTPTNHLHWKLRMKVFCVCCASTSHSGEKPVT 180  
Db 121 KFSEKF-RYSAFSLGYEFHAGHEYYISTPTNHLHWKLRMKVFCVCCASTSHSGEKPVT 179

Qy 181 LPQFTMGPNVKINLVLEDFEGENPOVPKLEKSIGTSPKREHLPLAVGIAFFLMTFLAS 238  
Db 180 LPQFTMGPNVKINLVLEDFEGENPOVPKLEKSIGTSPKREHLPLAVGIAFFLMTFLAS 237

RESULT 10  
US-08-229-402-7  
; Sequence 7, Application US/08229402  
; GENERAL INFORMATION:  
; APPLICANT: Davis, et al.  
; TITLE OF INVENTION: EPH Family Ligands  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
; STREET: 777 Old Saw Mill River Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/229,402  
; FILING DATE: 12-APR-1994  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/222,075  
; FILING DATE: 04-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/144,992  
; FILING DATE: 15-NOV-1993  
; APPLICATION NUMBER: US 07/736,559  
; FILING DATE: 26-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kempler Ph.D., Gail M.  
; REGISTRATION NUMBER: 32,143  
; REFERENCE/DOCKET NUMBER: REG 280  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 914-345-7400  
; TELEFAX: 914-347-2113  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-229-402-7

Query Match 97.3%; Score 1266; DB 6; Length 234;  
Best Local Similarity 98.3%; Pred. No. 8.8e-120;  
Matches 234; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 MAAAPLLLLLVLPVPLPLLAQPGGALGNHRHAYVWNSNOHLRREGYTVQVNVNDYLD 60  
Db 1 MAAAPLLLLLVLPVPLPLLAQPGGALGNHRHAYVWNSNOHLRREGYTVQVNVNDYLD 60

Qy 61 IYCPHYNSSGVGPGAGPGGAEQYVLYMYVRNGYRTCNASQGFKRWECPHAPHSP 120  
Db 61 IYCPHYNSSGVGPGAGPGGAEQYVLYMYVRNGYRTCNASQGFKRWECPHAPHSP 116

Qy 121 KFSEKFORYSAFSLGYEFHAGHEYYISTPTNHLHWKLRMKVFCVCCASTSHSGEKPVT 180  
Db 117 KFSEKFORYSAFSLGYEFHAGHEYYISTPTNHLHWKLRMKVFCVCCASTSHSGEKPVT 176

Qy 181 LPQFTMGPNVKINLVLEDFEGENPOVPKLEKSIGTSPKREHLPLAVGIAFFLMTFLAS 238  
Db 177 LPQFTMGPNVKINLVLEDFEGENPOVPKLEKSIGTSPKREHLPLAVGIAFFLMTFLAS 234

RESULT 11

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US-08-327-423-5
; Sequence 5, Application US/08327423
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
; TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,423
; FILING DATE: 21-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/299,567
; FILING DATE: 01-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler, Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
US-08-327-423-5

Query Match 96.9%; Score 1261; DB 7; Length 234;
Best Local Similarity 97.9%; Pred. No. 2.8e-119;
Matches 233; Conservative 1; Indels 4; Gaps 1;

Qy 1 MAAPLLLLLLVPVPLPPLLAQGGGALGNRHAYWNSSNOHLRREGYTVQVNVNDYLD 60
Db 1 MAAPLLLLLLVPVPLPPLPPLLAQGGGALGNRHAYWNSSNOHLRREGYTVQVNVNDYLD 60
Qy 61 IYCPHNSGVGPGAGPGGGAGQYVLYMYSRNGYRTCNASQGFKEWECNRPAPHSP 120
Db 61 IYCPHNSG---GAGPGGGAGQYVLYMYSRNGYRTCNASQGFKEWECNRPAPHSP 116
Qy 121 KFSEKQRYSAFSLGYEFHAGHEYIISTPTNHLHWKCLRMKVFVCCASTSHSGEKVP 180
Db 121 KFSEKQRYSAFSLGYEFHAGHEYIISTPTNHLHWKCLRMKVFVCCASTSHSGEKVP 176
Qy 181 LPQFTMGPNVINLDEFEENPOVPKLEKISGTSPKREHLPLAVGIAFFLMTFLAS 238
Db 177 LPQFTMGPNVINLDEFEENPOVPKLEKISGTSPKREHLPLAVGIAFFLMTFLAS 234

RESULT 12
US-08-730-700A-15
; Sequence 15, Application US/08730700A
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; TITLE OF INVENTION: Method of Activating a Novel Ligand
; TITLE OF INVENTION: Regulatory Pathway
; NUMBER OF SEQUENCES: 21
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Room 970
; STREET: 600 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1X5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,700A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,518
; FILING DATE: 13-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M.
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 416-586-3235
; TELEFAX: 416-586-3110
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-730-700A-15

Query Match 96.1%; Score 1250.5; DB 11; Length 233;
Best Local Similarity 97.9%; Pred. No. 3.3e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 5; Gaps 2;

Qy 1 MAAPLLLLLLVPVPLPPLLAQGGGALGNRHAYWNSSNOHLRREGYTVQVNVNDYLD 60
Db 1 MAAPLLLLLLVPVPLPPLPPLLAQGGGALGNRHAYWNSSNOHLRREGYTVQVNVNDYLD 60
Qy 61 IYCPHNSGVGPGAGPGGGAGQYVLYMYSRNGYRTCNASQGFKEWECNRPAPHSP 120
Db 61 IYCPHNSG---GAGPGGGAGQYVLYMYSRNGYRTCNASQGFKEWECNRPAPHSP 116
Qy 121 KFSEKQRYSAFSLGYEFHAGHEYIISTPTNHLHWKCLRMKVFVCCASTSHSGEKVP 180
Db 121 KFSEKQRYSAFSLGYEFHAGHEYIISTPTNHLHWKCLRMKVFVCCASTSHSGEKVP 175
Qy 181 LPQFTMGPNVINLDEFEENPOVPKLEKISGTSPKREHLPLAVGIAFFLMTFLAS 238
Db 176 LPQFTMGPNVINLDEFEENPOVPKLEKISGTSPKREHLPLAVGIAFFLMTFLAS 233

RESULT 13
US-09-621-595-15
; Sequence 15, Application US/09621595
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; TITLE OF INVENTION: Method of Activating a Novel Ligand
; TITLE OF INVENTION: Regulatory Pathway
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Room 970
; STREET: 600 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1X5
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/621,595  
FILING DATE: 21-Jul-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/730,700  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurydyk, Linda M.  
REGISTRATION NUMBER: 34,971  
REFERENCE/DOCKET NUMBER: 3153-196  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 416-586-3235  
TELEFAX: 416-586-3110  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-621-595-15

Query Match 96.1%; Score 1250.5; DB 20; Length 233;  
Best Local Similarity 97.9%; Pred. No. 3.3e-118;  
Matches 233; Conservative 0; Mismatches 0; Indels 5; Gaps 2;  
QY 1 MAAAPLLLLLLVPVPLLLAOGPGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
DB 1 MAAAPLLLLLLVPVPLLLAOGPGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
QY 61 IYCPHYNSSGGVPGAGPGGAGQYVLYMYVSRNGYRTCNASQGFKRWEKNRPHAPHSP 120  
DB 61 IYCPHYNSSGGVPGGAGQYVLYMYVSRNGYRTCNASQGFKRWEKNRPHAPHSP 116  
QY 121 KFSEKFORYSAFSLGYEFHAGHEYYIISTPTNHLHWKCLRMKVFCVCCASTSHSGEKP 180  
DB 117 KFSEKFORYSAFSLGYEFHAGHEYYIISTPTNHLHWKCLRMKVFCVCCASTSHSGEKP 175  
QY 181 LPQFTMGPNVKINLVDFEGENPOVPKLEKSISGTSFKREHLPLAVGIAFFLMTFLAS 238  
DB 176 LPQFTMGPNVKINLVDFEGENPOVPKLEKSISGTSFKREHLPLAVGIAFFLMTFLAS 233

RESULT 14  
US-09-214-631-7  
Sequence 7, Application US/09214631  
GENERAL INFORMATION:  
APPLICANT: Holland, Sacha  
APPLICANT: Mbamalu, Geraldine  
APPLICANT: Pawson, Tony  
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED  
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR  
FILE REFERENCE: 11757.23USWO  
CURRENT FILING DATE: 1999-03-12  
EARLIER APPLICATION NUMBER: PCT/CA97/00473  
EARLIER FILING DATE: 1997-07-04  
EARLIER APPLICATION NUMBER: 60/021,272  
EARLIER FILING DATE: 1996-07-05  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 233  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-214-631-7

Query Match 94.4%; Score 1227.5; DB 16; Length 233;  
Best Local Similarity 96.2%; Pred. No. 7.2e-116;  
Matches 229; Conservative 0; Mismatches 4; Indels 5; Gaps 2;  
QY 1 MAAAPLLLLLLVPVPLLLAOGPGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
DB 1 MAAAPLLLLLLVPVPLLLAOGPGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDYLD 60  
QY 61 IYCPHYNSSGGVPGAGPGGAGQYVLYMYVSRNGYRTCNASQGFKRWEKNRPHAPHSP 120  
DB 61 IYCPHYNSSGGVPGAGPGGAGQYVLYMYVSRNGYRTCNASQGFKRWEKNRPHAPHSP 115  
QY 121 KFSEKFORYSAFSLGYEFHAGHEYYIISTPTNHLHWKCLRMKVFCVCCASTSHSGEKP 180  
DB 116 KFSEKFORYSAFSLGYEFHAGHEYYIISTPTNHLHWKCLRMKVFCVCCASTSHSGEKP 175  
QY 181 LPQFTMGPNVKINLVDFEGENPOVPKLEKSISGTSFKREHLPLAVGIAFFLMTFLAS 238  
DB 176 LPQFTMGPNVKINLVDFEGENPOVPKLEKSISGTSFKREHLPLAVGIAFFLMTFLAS 233

RESULT 15  
US-60-212-656-335  
Sequence 335, Application US/60212656  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,  
AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CL000673  
CURRENT APPLICATION NUMBER: US/60/212,656  
CURRENT FILING DATE: 2000-06-19  
NUMBER OF SEQ ID NOS: 795  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 335  
LENGTH: 776  
TYPE: PRT  
ORGANISM: HUMAN  
US-60-212-656-335

Query Match 56.8%; Score 739; DB 26; Length 776;  
Best Local Similarity 65.0%; Pred. No. 1.6e-65;  
Matches 145; Conservative 17; Mismatches 43; Indels 18; Gaps 5;  
QY 23 QGPGGALGNRHAV-YWNSSNO----HLRREGYTVQVNVNDYLDIYCPHYNSSGGVPGAGP 77  
DB 565 KGDWGRVGPQPGTKVWSKGQTPILKLLRGDAVVELGLNDYLDIVCPHYE-----GP 616  
QY 78 GPGGAGQYVLYMYVSRNGYRTCNAS--QGFKRWEKNRPHAPHSPKIFSEKFORYSAFSLG 135  
DB 617 GPPEGPETFALYMDWPGYESCQAEPYAKRWVCS---LPFGHVQFSEKIQRETPTFSLG 673  
QY 136 YEFHAGHEYYIISTPTNHLHWKCLRMKVFCVCCASTSHSGEKPVPPLPQFTMGPNVKINVL 195  
DB 674 FEFPLGETYYIISTPTNHLHWKCLRMKVFCVCCASTSHSGEKPVPPLPQFTMGPNVKINVL 733  
QY 196 EDFEGENPOVPKLEKSISGTSFKREHLPLAVGIAFFLMTFLAS 238  
DB 734 EDFEGENPOVPKLEKSISGTSFKREHLPLAVGIAFFLMTFLAS 776

Search completed: September 28, 2002, 01:43:26  
Job time: 891 sec

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RESULT          6
PCT-US02-24563-288
; Sequence 288, Application PC/TUS0224563
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gadowski, Paul J.
; APPLICANT: Gurney, Austin L.

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```

RESULT 7
US-10-121-049-288
; Sequence 288, Application US/10121049
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Baresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.

```

```
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC17
; CURRENT APPLICATION NUMBER: US/10/121.049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-288

Query Match      29.0%; Score 377.5; DB 6; Length 204;
Best Local Similarity 40.9%; Pred. No. 5.2e-28;
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;

Qy 19 PLLAAGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYDIYCPHYNSSGVGPGAGPG 78
Db 7 PLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA----- 59
Qy 79 PGGAGQVLYVMVSRNGYRTCN-ASQGFKRWCNRPAPHSPIKFSEKFORYSAFSLGYE 137
Db 60 -DAAMEQVILYVEHEEYQLCPOQSKDQVRWCNRPASAKHPEKLFSEKFORPTPTLGKE 118
Qy 138 FHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKVPVTLPOFTMGPNVKINVLED 197
Db 119 FKEGHSYIYISKPIHQHEDRLRLKVTV-SGKITHS-----PQAHNDNPOEKRLAADD 169
Qy 198 FEGENPQVPLEKSIKSGTSPKREHLPLA 225
Db 170 -----PEVRVLHSGHSAAPRL--FPLA 190

RESULT 9
US-10-121-053-288
; Sequence 288, Application US/10121053
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC23
; CURRENT APPLICATION NUMBER: US/10/121.053
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-053-288

Query Match      29.0%; Score 377.5; DB 6; Length 204;
Best Local Similarity 40.9%; Pred. No. 5.2e-28;
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;

Qy 19 PLLAAGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYDIYCPHYNSSGVGPGAGPG 78
Db 7 PLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA----- 59
Qy 79 PGGAGQVLYVMVSRNGYRTCN-ASQGFKRWCNRPAPHSPIKFSEKFORYSAFSLGYE 137
Db 60 -DAAMEQVILYVEHEEYQLCPOQSKDQVRWCNRPASAKHPEKLFSEKFORPTPTLGKE 118
Qy 138 FHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKVPVTLPOFTMGPNVKINVLED 197
Db 119 FKEGHSYIYISKPIHQHEDRLRLKVTV-SGKITHS-----PQAHNDNPOEKRLAADD 169
Qy 198 FEGENPQVPLEKSIKSGTSPKREHLPLA 225
Db 170 -----PEVRVLHSGHSAAPRL--FPLA 190

RESULT 8
US-10-121-050-288
; Sequence 288, Application US/10121050
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC20
; CURRENT APPLICATION NUMBER: US/10/121.050
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
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; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-050-288

Query Match      29.0%; Score 377.5; DB 6; Length 204;
Best Local Similarity 40.9%; Pred. No. 5.2e-28;
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;

Qy 19 PLLAAGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYDIYCPHYNSSGVGPGAGPG 78
Db 7 PLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA----- 59
Qy 79 PGGAGQVLYVMVSRNGYRTCN-ASQGFKRWCNRPAPHSPIKFSEKFORYSAFSLGYE 137
Db 60 -DAAMEQVILYVEHEEYQLCPOQSKDQVRWCNRPASAKHPEKLFSEKFORPTPTLGKE 118
Qy 138 FHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKVPVTLPOFTMGPNVKINVLED 197
Db 119 FKEGHSYIYISKPIHQHEDRLRLKVTV-SGKITHS-----PQAHNDNPOEKRLAADD 169
Qy 198 FEGENPQVPLEKSIKSGTSPKREHLPLA 225
Db 170 -----PEVRVLHSGHSAAPRL--FPLA 190

RESULT 9
US-10-121-053-288
; Sequence 288, Application US/10121053
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC23
; CURRENT APPLICATION NUMBER: US/10/121.053
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-053-288

Query Match      29.0%; Score 377.5; DB 6; Length 204;
Best Local Similarity 40.9%; Pred. No. 5.2e-28;
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;

Qy 19 PLLAAGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYDIYCPHYNSSGVGPGAGPG 78
Db 7 PLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA----- 59
Qy 79 PGGAGQVLYVMVSRNGYRTCN-ASQGFKRWCNRPAPHSPIKFSEKFORYSAFSLGYE 137
Db 60 -DAAMEQVILYVEHEEYQLCPOQSKDQVRWCNRPASAKHPEKLFSEKFORPTPTLGKE 118
Qy 138 FHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGEKVPVTLPOFTMGPNVKINVLED 197
Db 119 FKEGHSYIYISKPIHQHEDRLRLKVTV-SGKITHS-----PQAHNDNPOEKRLAADD 169
Qy 198 FEGENPQVPLEKSIKSGTSPKREHLPLA 225
Db 170 -----PEVRVLHSGHSAAPRL--FPLA 190
```

Db 60 -DAAMEQYILYVEHEEYQLCQPSQDQVRWQCNRRSAKHGPEKLSKFORFTPTLIGKE 118  
QY 138 FHAGHEYYIISTPTNHLHWKLRMKVFCVCCASTSHSSEKVPVTLPOFTMGPNVKINVL 197  
Db 119 FKEGHSYYIISKPIHQHEDRCRLKVTV-SGKITHS-----POAHDNPQEKRLAADD 169  
QY 198 FEGENPOVPKLEKSISGTSFKREHLPLA 225  
Db 170 -----PEVRVLHSGHSAAPRL--FPLA 190

## RESULT 10

US-10-121-043-288  
; Sequence 288, Application US/10121043  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C5  
; CURRENT APPLICATION NUMBER: US/10/121,043  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 288  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-121-043-288

Query Match 29.0%; Score 377.5; DB 6; Length 204;  
Best Local Similarity 40.9%; Pred. No. 5.2e-28;  
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;

QY 19 PLLAQPGGALGNRHAYWNSSNOHLRREGYTVQVNVNDYLDIYCPHYNSGSGVGPAGPG 78  
Db 7 PLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTHVQLNDYDIICPHYEDHSA----- 59  
QY 79 PGGAEQYVLYMVSRRNGYRTCN-ASOGFKRWCNRPAPHSPKFKSFQRYSAFSLGYE 137  
Db 60 -DAAMEQYILYVEHEEYQLCQPSQDQVRWQCNRRSAKHGPEKLSKFORFTPTLIGKE 118  
QY 138 FHAGHEYYIISTPTNHLHWKLRMKVFCVCCASTSHSSEKVPVTLPOFTMGPNVKINVL 197  
Db 119 FKEGHSYYIISKPIHQHEDRCRLKVTV-SGKITHS-----POAHDNPQEKRLAADD 169  
QY 198 FEGENPOVPKLEKSISGTSFKREHLPLA 225  
Db 170 -----PEVRVLHSGHSAAPRL--FPLA 190

## RESULT 11

US-10-121-044-288  
; Sequence 288, Application US/10121044  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C5  
; CURRENT APPLICATION NUMBER: US/10/121,044  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 288  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-121-044-288

Query Match 29.0%; Score 377.5; DB 6; Length 204;  
Best Local Similarity 40.9%; Pred. No. 5.2e-28;  
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;

QY 19 PLLAQPGGALGNRHAYWNSSNOHLRREGYTVQVNVNDYLDIYCPHYNSGSGVGPAGPG 78  
Db 7 PLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTHVQLNDYDIICPHYEDHSA----- 59  
QY 79 PGGAEQYVLYMVSRRNGYRTCN-ASOGFKRWCNRPAPHSPKFKSFQRYSAFSLGYE 137  
Db 60 -DAAMEQYILYVEHEEYQLCQPSQDQVRWQCNRRSAKHGPEKLSKFORFTPTLIGKE 118  
QY 138 FHAGHEYYIISTPTNHLHWKLRMKVFCVCCASTSHSSEKVPVTLPOFTMGPNVKINVL 197  
Db 119 FKEGHSYYIISKPIHQHEDRCRLKVTV-SGKITHS-----POAHDNPQEKRLAADD 169  
QY 198 FEGENPOVPKLEKSISGTSFKREHLPLA 225  
Db 170 -----PEVRVLHSGHSAAPRL--FPLA 190

RESULT 12  
US-10-121-047-288  
; Sequence 288, Application US/10121047  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C5  
; CURRENT APPLICATION NUMBER: US/10/121,047  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 288  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-121-047-288

```

; FILE REFERENCE: P3330RIC4
; CURRENT APPLICATION NUMBER: US/10/121.047
; CURRENT FILING DATE: 2002-04-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-047-288

Query Match          29.0%; Score 377.5; DB 6; Length 204;
Best Local Similarity 40.9%; Pred. No. 5.2e-28;
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;

Qy 19 PLLAQGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
Db 7 PLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA----- 59
Qy 79 PGGAGQVLYVMVSRNGYRTCN-ASQGFKRWECNRPAPHSPKIFSEKFORYSAFSLGYE 137
Db 60 -DAAMEQVILYLVHEEYQLCPQSQKQDVRCNRPSSAKHGPEKLSKFKRFTPTTLGKE 118
Qy 138 FHAGHEYIYISTPTNHLHWKCLRMKVFVCCASTSHSGEKPVTPLPQFTMGPNVKINVL 197
Db 119 FKEGHSYIYISKPIHQHEDRCLRLKVTV--SGKITHS-----PQAHNDNPQEKRLAADD 169
Qy 198 FEGENPQVPKLEKSISGTSKPREHLPLA 225
Db 170 -----PEVRLHSGHSAAPRL--FPLA 190

RESULT 13
US-10-121-054-288
; Sequence 288, Application US/10121054
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC14
; CURRENT APPLICATION NUMBER: US/10/121.054
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-054-288

Query Match          29.0%; Score 377.5; DB 6; Length 204;
Best Local Similarity 40.9%; Pred. No. 5.2e-28;
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;

Qy 19 PLLAQGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
Db 7 PLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA----- 59
Qy 79 PGGAGQVLYVMVSRNGYRTCN-ASQGFKRWECNRPAPHSPKIFSEKFORYSAFSLGYE 137
Db 60 -DAAMEQVILYLVHEEYQLCPQSQKQDVRCNRPSSAKHGPEKLSKFKRFTPTTLGKE 118
Qy 138 FHAGHEYIYISTPTNHLHWKCLRMKVFVCCASTSHSGEKPVTPLPQFTMGPNVKINVL 197
Db 119 FKEGHSYIYISKPIHQHEDRCLRLKVTV--SGKITHS-----PQAHNDNPQEKRLAADD 169
Qy 198 FEGENPQVPKLEKSISGTSKPREHLPLA 225
Db 170 -----PEVRLHSGHSAAPRL--FPLA 190

RESULT 14
US-10-121-056-288
; Sequence 288, Application US/10121056
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC25
; CURRENT APPLICATION NUMBER: US/10/121.056
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-056-288

Query Match          29.0%; Score 377.5; DB 6; Length 204;
Best Local Similarity 40.9%; Pred. No. 5.2e-28;
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;

Qy 19 PLLAQGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
Db 7 PLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA----- 59
Qy 79 PGGAGQVLYVMVSRNGYRTCN-ASQGFKRWECNRPAPHSPKIFSEKFORYSAFSLGYE 137
Db 60 -DAAMEQVILYLVHEEYQLCPQSQKQDVRCNRPSSAKHGPEKLSKFKRFTPTTLGKE 118
Qy 138 FHAGHEYIYISTPTNHLHWKCLRMKVFVCCASTSHSGEKPVTPLPQFTMGPNVKINVL 197
Db 119 FKEGHSYIYISKPIHQHEDRCLRLKVTV--SGKITHS-----PQAHNDNPQEKRLAADD 169
Qy 198 FEGENPQVPKLEKSISGTSKPREHLPLA 225
Db 170 -----PEVRLHSGHSAAPRL--FPLA 190

RESULT 15
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US-10-121-057-288  
; Sequence 288, Application US/10121057  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C13  
; CURRENT APPLICATION NUMBER: US/10/121,057  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 288  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-121-057-288

Query Match 29.0%; Score 377.5; DB 6; Length 204;  
Best Local Similarity 40.9%; Pred. No. 5.2e-28;  
Matches 85; Conservative 20; Mismatches 78; Indels 25; Gaps 6;  
QY 19 PLLAOGPGGALGNRHVYWNSSNQHLLRREGYTVQVNVNDYDIYCPHYNSSGVGPGAGPG 78  
Db 7 PLLGLCCSLAAADRHVFNWSSNPKFRNEDYTHVQLNDYVDIICPHYEDHSA----- 59  
QY 79 PGCGAQYVLYVYVRNGYFTCN-ASQGFKRWECNRPHAPHSPIKFSEKFORYSAFSLGYE 137  
Db 60 -DAAMEQYILYVEHEEYQLCQPSKQDQVRWCNRPNSAKHGEKLEKFORFTPTLGKE 118  
QY 138 FHAGHEYIYISTETHNLHWKLRMYVCCASTSHSCEKVPVTLPQFTMGPNVKINVL 197  
Db 119 FKEGHSTYIYISKPIHQHEDCLRLKVTV-SGKITHS-----POAHDNPQEKRLAAD 169  
QY 198 FEGENQVPKLEKSIQTSFKREHLPLA 225  
Db 170 -----PEVRVLHSHGHSAPRL--FPLA 190

Search completed: September 28, 2002, 01:45:54  
Job time: 619 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2002, 00:26:55 ; Search time 49.23 Seconds  
(without alignments)  
464.539 Million cell updates/sec

Title: US-09-904-954-2

Perfect score: 1301

Sequence: 1 MAAPLPLLLLVPPVLLPL.....REHPLAVGIAFFLMTFLAS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	238	2 I38849	LERK-3 - human
2	437	33.6	209	2 A54984	ELF-1 protein prec
3	434	33.4	213	2 JF0322	ephrin-A2 - human
4	415.5	31.9	228	2 I58170	LERK-7 precursor -
5	404.5	31.1	228	2 A57084	repulsive axon gui
6	390	30.0	205	2 A36377	B61 protein precu
7	364.5	28.0	201	2 I38850	LERK-4 - human
8	171.5	13.2	333	2 I84743	hepatoma transmem
9	171.5	13.2	336	2 I49766	hepatoma transmem
10	148.5	11.4	346	2 S46993	elk ligand - human
11	143.5	11.0	462	2 T32645	hypothetical prote
12	139.5	10.7	345	2 I48780	Stral/Eplg2 protei
13	132.5	10.2	345	2 I58406	LERK-2 - rat
14	100	7.7	356	2 T40265	hypothetical zinc-
15	91	7.0	2206	1 GNNY27	genome polyprotein
16	88.5	6.8	1024	2 E50678	beta-D-galactosida
17	88.5	6.8	1024	2 A85529	beta-D-galactosida
18	87	6.7	817	2 T21336	hypothetical prote
19	85.5	6.6	709	2 T28712	hypothetical prote
20	84	6.5	1027	2 T19173	hypothetical prote
21	83.5	6.4	488	2 S67744	hypothetical prote
22	82.5	6.3	432	2 A25483	env polyprotein, r
23	82.5	6.3	466	1 TWFF	transcription fact
24	82	6.3	237	2 T19914	hypothetical prote
25	82	6.3	334	2 T16772	hypothetical prote
26	82	6.3	376	2 B84463	hypothetical prote
27	82	6.3	728	2 A48830	probable transcrip
28	82	6.3	1144	2 A75132	hypothetical prote
29	81.5	6.3	1173	2 I50620	prockr2 - chicken

30 81 6.2 457 2 T19109  
31 81 6.2 1613 2 S39059  
32 81 6.2 1647 2 S45252  
33 79.5 6.1 434 2 E72410  
34 79 6.1 612 2 A54282  
35 79 6.1 859 1 VCLJMN  
36 78.5 6.0 202 2 T01605  
37 78.5 6.0 498 2 B84789  
38 78.5 6.0 1024 1 GBEC  
39 78.5 6.0 1291 2 T13389  
40 78 6.0 321 2 I38238  
41 78 6.0 328 1 S05426  
42 78 6.0 700 2 A32392  
43 78 6.0 2206 1 GNNY4P  
44 78 6.0 2206 2 S03822  
45 77.5 6.0 570 2 H90370

#### ALIGNMENTS

##### RESULT 1

I38849

LERK-3 - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 29-Sep-1999

C:Accession: I38849

R:Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.

Oncogene 10, 299-306, 1995

A:Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs en

A:Reference number: I38849; MUID:95140419

A:Accession: I38849

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-238 <RES>

A:Cross-references: EMBL:U14187; NID:9642832; PIDN:AAC50078.1; PID:9642833

C:Genetics:

A:Gene: GDB:EPLG3

A:Cross-references: GDB:438336; OMIM:601381

A:Map position: lq21-lq22

C:Superfamily: axon guidance signal protein

Query Match 100.0%; Score 1301; DB 2; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.7e-114;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAPLPLLLLVPPVLLPLLAQPGGALGNRHAYVWNSNQHLREGYTVQVNVNDYLD 60

Db 1 MAAPLPLLLLVPPVLLPLLAQPGGALGNRHAYVWNSNQHLREGYTVQVNVNDYLD 60

Qy 61 IYCPHYNSGVGPGAGPGGAEQVLYVMYSRNGYRTCNASQGFKECNRPAPHSP 120

Db 61 IYCPHYNSGVGPGAGPGGAEQVLYVMYSRNGYRTCNASQGFKECNRPAPHSP 120

Qy 121 KFSEKQRYSAFSLGYEFHAGHEYIYSTPTNLHWKCLRMKFVCCASTSHSGKPVPT 180

Db 121 KFSEKQRYSAFSLGYEFHAGHEYIYSTPTNLHWKCLRMKFVCCASTSHSGKPVPT 180

Qy 181 LPQFTMGPNVKINLVLEFEGENPQVPKLEKISGTSFKREHLPLAVGTAFFLMTFLAS 238

Db 181 LPQFTMGPNVKINLVLEFEGENPQVPKLEKISGTSFKREHLPLAVGTAFFLMTFLAS 238

##### RESULT 2

A54984

ELF-1 protein precursor - mouse

N:Alternate names: Cek7 ligand

C:Species: Mus musculus (house mouse)

C>Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 29-Sep-1999

C:Accession: A54984; A55873

R:Cheng, H.J.; Flanagan, J.G.

Cell 79, 157-168, 1994

[illegible]



```

RESULT 7
I38850
LERK-4 - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C:Accession: I38850
R:Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Tespe, M.;

```

```

RESULT      7
I38850
LERK-4 - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C:Accession: I38850
R:Kozlosky, C.J.: Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.:

```

[illegible]

```
RESULT 9
I49766
hepatoma transmembrane kinase ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49766
R:Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A:Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin
A:Reference number: I49766; MUID:95199254
A:Accession: I49766
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-336 <RES>
A:Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678
C:Genetics:
A:Gene: HTK

Query Match 13.2%; Score 171.5; DB 2; Length 336;
Best Local Similarity 28.3%; Pred. No. 2.4e-08;
Matches 62; Conservative 27; Mismatches 101; Indels 29; Gaps 8;

QY 35 VYWNSSN-OHLRREGYTVQVNVNDYDIYCPHYNSGVGPGAGPGGGAGQYVLYMYSR 93
DB 36 IYWNSSNKFPLGQGLVLYPQIGDKLDIICPKVDKTVGQ-----YEEKYVMYDK 86

QY 94 NGYRTCN-ASQGFKRWCNRPAPHSPIKFSEKFORYSAFSLGVEFHAGHEYYIYSTPTH 152
DB 87 DOADRCTIKENTPLNLCAR---PQDVKFTIKFQFSPNLWGLEFQKNKDYIISTSG 143

QY 153 NLH-----WKCLRKMKVFVCC---ASTSHSGEKVPPT-LPQFTMGPNVKINYLEDFE 199
DB 144 SLEGLDNEGGVCOTRAMKILMKVQDASSAGSARNHGPTRRPELEAGTNGRSSTSPFV 203

QY 200 GENPOVPKLEKSI--SGTSPKREHLPLAVGIAFFLMTFL 236
DB 204 KPNGSSTDGNAGHSGNLLGSEVALFAGIASGCIIFI 242

RESULT 10
S46993
elk ligand - human
C:Species: Homo sapiens (man)
C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C:Accession: S46993
R:Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozl
EMBO J. 13, 3757-3762, 1994
A:Title: Molecular characterization of a family of ligands for eph-related tyrosine kin
A:Reference number: S46993; MUID:94349923
A:Accession: S46993
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-346 <BEC>
A:Cross-references: GB:U09304; NID:g538366; PIDN:AAA53093.1; PID:g538367

Query Match 11.4%; Score 148.5; DB 2; Length 346;
Best Local Similarity 26.4%; Pred. No. 3.5e-06;
Matches 55; Conservative 26; Mismatches 90; Indels 37; Gaps 7;

QY 31 NRHAYVWNSSN-OHLRREGYTVQVNVNDYDIYCPHYNSGVGPGAGPGGGAGQYVLY 89
DB 31 NLEPVSWSNLNPKFLSGGLGYTPYKIGDKLDIICPRAEA-----GRPYEYKLY 79

QY 90 MYSRNGYTCN-ASQGFKRWCNRPAPHSPIKFSEKFORYSAFSLGVEFHAGHEYYIIS 148
DB 80 LYVRPQAAACSTVLPDNLVTCNR---PEQIRFTIKFQFSPNVMGLEFKHHDDYYITS 136

QY 149 TPTHNLH-----WKCLRKMKVFVCCA-----STSHSGEKVPPTLPQFTMG 188
DB 137 TSNGLSLENGREGGVCRTMTMKILMKVQDQPNVTPQLITSRPSKEADNTVMKATQAP 196
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QY 189 NVKINVLDFEGENPOVPKLEKSISGTS 216
DB 197 GSR-GSLGSDGKHETVQNEEKSGPGAS 223

RESULT 11
T32645
hypothetical protein F56A11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32645
R:Gattung, S.; Goela, D.; Harper, M.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid F56A11.
A:Reference number: Z21204
A:Accession: T32645
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-462 <GAT>
A:Cross-references: EMBL:AF038619; PIDN:AAB92075.1; GSPDB:GN00022; CESP:F56A11.3
A:Experimental source: strain Bristol N2; clone F56A11
C:Genetics:
A:Gene: CESP:F56A11.3
A:Map position: 4
A:Introns: 37/3; 69/2; 103/2; 220/1; 388/1; 412/3

Query Match 11.0%; Score 143.5; DB 2; Length 462;
Best Local Similarity 23.1%; Pred. No. 1.5e-05;
Matches 54; Conservative 30; Mismatches 93; Indels 57; Gaps 10;

QY 26 GGALGNRHAYVWNSSNQHLLRREGYTVQVNVNDYDIYCPHYNSGVGPGAGPGGGAG 85
DB 86 GLAAADEHIVYWNSTNSLFRNRQPTIEVRMGDVVRVFCPD-NEEGRNDG-----EY 135

QY 86 VLYVWVSRNGYTC-----NASQGFKRWCNRPAPHSPISIK 121
DB 136 LIVVEVTEFAMDDCALESHSREVIRCAPEGTAEKVLRVTQQLSGRRDWMKKQVP--BKN 193

QY 122 FSEKFORYSAFSLGVEFHAGHEYYIYSTPT-----HNLHWKC-----LRMKVFVCCA 168
DB 194 VAQLIRQLNPNGKEYQPGQTYIYMTTSTGKANGTNRMYGLCESQNMRLSMKV---SA 250

QY 169 STSHSGEKVPPTLPQFTMGPNVKINVL---EDFEGENPOVPKLEKSISG-TSPK 218
DB 251 SOPHPTRR-APTROEDFVTTASAEIMGQDESDNDNAHLLPRDLEGSTNPK 303

RESULT 12
I48780
Stral/Eplg2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I48780; A55507; A55062; S52670
R:Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Doll
Dev. Biol. 170, 420-433, 1995
A:Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryona
A:Reference number: I48780; MUID:95377533
A:Accession: I48780
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-345 <RES>
A:Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859
R:Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A
Genomics 24, 127-132, 1994
A:Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene enc
A:Reference number: A55507; MUID:95203867
A:Accession: A55507
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <FLE>
A:Cross-references: GB:U07598
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R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.

J. Biol. Chem. 269, 26606-26609, 1994

A;Title: cDNA cloning and characterization of a ligand for the Cdk5 receptor protein-tyr

A;Reference number: A55062; MUID:95014510

A;Accession: A55062

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-89, T, 91-345 <SHA>

A;Cross-references: GB:012983; NID:g575928; PIDN:AAA53231.1; PID:g575929

C;Genetics:

A;Gene: EPLG2

Query Match 10.7%; Score 139.5; DB 2; Length 345;

Best Local Similarity 24.2%; Pred. No. 2.4e-05;

Matches 59; Conservative 27; Mismatches 87; Indels 71; Gaps 8;

Qy 4 APLLLLLLVPPVPLLLAQQGGALGNHAYVWSSN-OHLRREGYTVQVNVNDYLDIY 62

Db 15 AMVVTLCLRLATPLAK-----NLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy 63 CPHYNSSGVGPGAGPGGGAEQVLYVW-----SRNGYRTCNASQGFKRWEC 110

Db 64 CPRAEA-----GRPEYKLYLVRPEQAACSTVLDPNVLVTCN----- 102

Qy 111 NRPHAPHSPIKSEKFORYSAFSLGYPFHAGHEYIYSTPTTNLH-----WKCLRM 161

Db 103 ----KPHQEIIRFTIKQFESPNYNGLEPKKYHDVYITSTNSGLEGNREGGVCRTRTM 158

Qy 152 KVFVCCA-----STSHSGEKVPPTLPQFTMGPNVKINLVDFEGENPOVPKLEK 210

Db 159 KIVKMGQDPNAVTPTEQLTTSRPSKESDNTVKTATQAPG--RGSQSDSGKHETVNOQEK 216

Qy 211 SISG 214

Db 217 SGPG 220

Query Match 7.7%; Score 100; DB 2; Length 356;

Best Local Similarity 19.0%; Pred. No. 0.13;

Matches 42; Conservative 31; Mismatches 64; Indels 84; Gaps 8;

Qy 35 VYWNSSNOHLRREGYTVQVNVNDYLDIYCPHYNSGVGPGAGPGGGAEQVLYVWVS- 93

Db 161 LYWNKSVLLKKRFLKEVG-NSPSAVYCRYNANGI-----CGKGAACRFVHEPTRK 212

Qy 94 -----NGYRTCN-----ASQGFKRMECNRPAPHSPKIFKSE-----K 125

Db 213 TICPKFLNGRCNKAEDCNLSHELDPRIACRYFLGKCNPNCRVYVHIHSENAPICFE 272

Qy 126 FORTSASLSGVEFHAGHEYIYSTPTTNLH-WKCLRMKVFVCCASTSHSGEKVPPTLPQF 184

Db 273 FAKYFCBELG-----TSCKNQHLQCTDAMFGC----- 302

Qy 185 TMGNPVKINLVDFEGENPOVPKLEKISGTSKPREHLPLA 225

Db 303 -----NNPQCSLYHGAVSADVPQTEAPIS 327

RESULT 13

158406

LERK-2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999

C;Accession: 158406

R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Hollin

Oncogene 9, 3241-3248, 1994

A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conser

A;Reference number: 158406; MUID:95022634

A;Accession: 158406

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-345 <RES>

A;Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119

C;Genetics:

A;Gene: Ep1g2

Query Match

Best Local Similarity 10.2%; Score 132.5; DB 2; Length 345;

Matches 58; Conservative 27; Mismatches 88; Indels 71; Gaps 8;

Qy 4 APLLLLLLVPPVPLLLAQQGGALGNHAYVWSSN-OHLRREGYTVQVNVNDYLDIY 62

Db 15 AMVVTLCLRLATPLAK-----NLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy 63 CPHYNSSGVGPGAGPGGGAEQVLYVW-----SRNGYRTCNASQGFKRWEC 110

Db 64 CPRAEA-----GRPEYKLYLVRPEQAACSTVLDPNVLVTCN----- 102

Qy 111 NRPHAPHSPIKSEKFORYSAFSLGYPFHAGHEYIYSTPTTNLH-----WKCLRM 161

Db 103 ----KPHQEIIRFTIKQFESPNYNGLEPKKYHDVYITSTNSGLEGNREGGVCRTRTM 158

Qy 162 KVFVCCA-----STSHSGEKVPPTLPQFTMGPNVKINLVDFEGENPOVPKLEK 210

Db 159 KIVKMGQDPNAVTPTEQLTTSRPSKESDNTVKTATQAPG--RGSQSDSGKHETVNOQEK 216

Qy 211 SISG 214

Db 217 SGPG 220

Query Match 7.7%; Score 100; DB 2; Length 356;

Best Local Similarity 19.0%; Pred. No. 0.13;

Matches 42; Conservative 31; Mismatches 64; Indels 84; Gaps 8;

Qy 35 VYWNSSNOHLRREGYTVQVNVNDYLDIYCPHYNSGVGPGAGPGGGAEQVLYVWVS- 93

Db 161 LYWNKSVLLKKRFLKEVG-NSPSAVYCRYNANGI-----CGKGAACRFVHEPTRK 212

Qy 94 -----NGYRTCN-----ASQGFKRMECNRPAPHSPKIFKSE-----K 125

Db 213 TICPKFLNGRCNKAEDCNLSHELDPRIACRYFLGKCNPNCRVYVHIHSENAPICFE 272

Qy 126 FORTSASLSGVEFHAGHEYIYSTPTTNLH-WKCLRMKVFVCCASTSHSGEKVPPTLPQF 184

Db 273 FAKYFCBELG-----TSCKNQHLQCTDAMFGC----- 302

Qy 185 TMGNPVKINLVDFEGENPOVPKLEKISGTSKPREHLPLA 225

Db 303 -----NNPQCSLYHGAVSADVPQTEAPIS 327

RESULT 14

T40265

hypothetical zinc-finger protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C;Accession: T40265

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.

submitted to the EMBL Data Library, October 1998

A;Reference number: 221868

A;Accession: T40265

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-356 <LYN>

A;Cross-references: EMBL:AL031854; PIDN:CAA21282.1; GSPDB:GN00067; SPDB:SPBC337.12

A;Experimental source: strain 972h-; cosmid C337

C;Genetics:

A;Gene: SPDB:SPBC337.12

A;Map position: 2

Query Match 7.7%; Score 100; DB 2; Length 356;

Best Local Similarity 19.0%; Pred. No. 0.13;

Matches 42; Conservative 31; Mismatches 64; Indels 84; Gaps 8;

Qy 35 VYWNSSNOHLRREGYTVQVNVNDYLDIYCPHYNSGVGPGAGPGGGAEQVLYVWVS- 93

Db 161 LYWNKSVLLKKRFLKEVG-NSPSAVYCRYNANGI-----CGKGAACRFVHEPTRK 212

Qy 94 -----NGYRTCN-----ASQGFKRMECNRPAPHSPKIFKSE-----K 125

Db 213 TICPKFLNGRCNKAEDCNLSHELDPRIACRYFLGKCNPNCRVYVHIHSENAPICFE 272

Qy 126 FORTSASLSGVEFHAGHEYIYSTPTTNLH-WKCLRMKVFVCCASTSHSGEKVPPTLPQF 184

Db 273 FAKYFCBELG-----TSCKNQHLQCTDAMFGC----- 302

Qy 185 TMGNPVKINLVDFEGENPOVPKLEKISGTSKPREHLPLA 225

Db 303 -----NNPQCSLYHGAVSADVPQTEAPIS 327

RESULT 15

GNV27

genome polyprotein - human poliovirus 3 (strain 23127)

A;Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; c

A-directed RNA polymerase (EC 2.7.7.48)

C;Species: human poliovirus 3

C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 16-Jul-1999

C;Accession: A27245

R;Hughes, P.J.; Evans, D.M.A.; Minor, P.D.; Schild, G.C.; Almond, J.W.; Stanway, G.

J. Gen. Virol. 67, 2093-2102, 1986

A;Title: The nucleotide sequence of a type 3 poliovirus isolated during a recent outb

A;Reference number: A27245; MUID:87010550

A;Accession: A27245

A;Molecule type: genomic RNA

A;Residues: 1-2206 <HUG>

A;Cross-references: GB:X04468; NID:g61112; PIDN:CAA28155.1; PID:g61113

C;Superfamily: poliovirus genome polyprotein

C;Keywords: coat protein; core protein; genome-linked protein; nucleotidyltransferase

F;1-69/Product: coat protein VP4 #status predicted <VP4>

F;70-340/Product: coat protein VP2 #status predicted <VP2>

F;341-578/Product: coat protein VP3 #status predicted <VP3>

F;579-878/Product: coat protein VP1 #status predicted <VP1>

F;879-1027/Product: core protein P2-3b #status predicted <P3B>

Search completed: September 28, 2002, 01:38:54  
Job time: 4319 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2002, 01:37:46 ; Search time 27.02 Seconds  
(without alignments)  
341.053 Million cell updates/sec

Title: US-09-904-954-2

Perfect score: 1301

Sequence: 1 NAAAPLLLLLLVPPVLLPL.....REHEPLAVGIAPFLMTFLAS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1301	100.0	238	1	EFA3_HUMAN	P52797	homo sapien
2	963	74.0	187	1	EFA3_MOUSE	O08545	mus musculus
3	437	33.6	209	1	EFA2_MOUSE	P52801	mus musculus
4	437	33.6	213	1	EFA2_HUMAN	O43921	homo sapien
5	426	32.7	195	1	EFA2_BRARE	P79727	brachydanio
6	421	32.4	200	1	EFA2_CHICK	P52802	gallus gall
7	415.5	31.9	228	1	EFA5_HUMAN	P52803	homo sapien
8	414.5	31.9	228	1	EFA5_MOUSE	O08543	mus musculus
9	414.5	31.9	228	1	EFA5_RAT	P97605	rattus norv
10	410	31.5	206	1	EFA4_MOUSE	O08542	mus musculus
11	404.5	31.1	228	1	EFA5_CHICK	P52804	gallus gall
12	397	30.5	228	1	EFA5_BRARE	P79728	brachydanio
13	390	30.0	205	1	EFA1_HUMAN	P20827	homo sapien
14	375.5	28.9	216	1	EFA1_XENLA	P52794	xenopus lae
15	374	28.7	205	1	EFA1_MOUSE	P52793	mus musculus
16	364.5	28.0	201	1	EFA4_HUMAN	P52798	homo sapien
17	362	27.8	205	1	EFA1_RAT	P97553	rattus norv
18	179	13.8	340	1	EFB3_HUMAN	O15768	homo sapien
19	177	13.6	340	1	EFB3_MOUSE	O35393	mus musculus
20	171.5	13.2	333	1	EFB2_HUMAN	P52799	homo sapien
21	171.5	13.2	336	1	EFB2_MOUSE	P52800	mus musculus
22	148.5	11.4	346	1	EFB1_HUMAN	P98172	homo sapien
23	147	11.3	332	1	EFB2_BRARE	O73874	brachydanio
24	139.5	10.7	345	1	EFB1_MOUSE	P52795	mus musculus
25	134	10.3	327	1	EFB1_XENLA	O13037	xenopus lae
26	132.5	10.2	345	1	EFB1_RAT	P52796	rattus norv
27	122.5	9.4	334	1	EFB1_CHICK	O73612	gallus gall
28	91	7.0	2206	1	POLG_POL32	P06209	poliovirus
29	88.5	6.8	894	1	ILF3_HUMAN	O12906	h interleuk
30	85	6.5	400	1	CASP_MOUSE	O9CY93	mus musculus
31	83.5	6.4	910	1	ILF3_RAT	Q9J113	rattus norv
32	82.5	6.32	432	1	ENV2_MOUSE	P11370	mus musculus
33	82.5	6.3	466	1	KRUP_DROME	P07247	drosophila

P48432 mus musculu  
Q10462 caenorhabdi  
Q921x4 mus musculu  
P51532 homo sapien  
P38159 homo sapien  
P05877 human immun  
P00722 escherichia  
Q92826 homo sapien  
P48431 homo sapien  
P54231 ovis aries  
P05315 solanum tub  
P13677 drosophila

34 82 6.3 319 1 SOX2\_MOUSE  
35 82 6.3 334 1 CAHX\_CAEEL  
36 81 6.2 911 1 ILF3\_MOUSE  
37 81 6.2 1647 1 SN24\_HUMAN  
38 79.5 6.1 391 1 ROG\_HUMAN  
39 79 6.1 856 1 ENV\_HVIMN  
40 78.5 6.0 1023 1 BGAL\_ECOLI  
41 78 6.0 284 1 HXBD\_HUMAN  
42 78 6.0 317 1 SOX2\_HUMAN  
43 78 6.0 320 1 SOX2\_SHEEP  
44 78 6.0 328 1 CHIT\_SOLTU  
45 78 6.0 700 1 KPC2\_DROME

#### ALIGNMENTS

RESULT 1  
ID EFA3\_HUMAN STANDARD; PRT; 238 AA.  
AC P52797;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand 3)  
DE (LERK-3) (EHK1 ligand) (EHK1-L).  
GN EFN3 OR EPLG3 OR LERK3 OR EFL-2.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95140419; PubMed=7838529;  
RA Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,  
RA Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,  
RA Cerretti D.P., Beckmann M.P.;  
RT "Ligands for the receptor tyrosine kinases hek and elk: isolation of  
RT cDNAs encoding a family of proteins.";  
RL Oncogene 10:299-306(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95063919; PubMed=7973638;  
RA Davis S., Gale N.W., Aldrich T.H., Maisonnier P.C., Lhotak V.,  
RA Pawson T., Goldfarb M., Yancopoulos G.D.;  
RT "Ligands for EPH-related receptor tyrosine kinases that require  
RT membrane attachment or clustering for activity.";  
RL Science 266:816-819(1994).  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKELETAL MUSCLE, SPLEEN,  
CC THYMUS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE, AND PERIPHERAL  
CC BLOOD LEUKOCYTES.  
CC -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL: U14187; AAC50078.1; -;  
DR EMBL: L37360; AAA52368.1; -;  
DR MIM: 601381; -;  
DR InterPro: IPR001799; Ephrin.  
DR Pfam: PF00812; Ephrin; 1.  
DR PRINTS: PR01347; EPHRIN.  
DR ProDom: PD002533; Ephrin; 1.  
DR PROSITE: PS01299; EPHRIN; 1.  
KW Glycoprotein; GPI-anchor; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 238  
FT EPHRIN-A3.

FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 71 74 MISSING (IN REF. 2).  
 SQ SEQUENCE 238 AA: 26350 MW; 8EFD6AE8FE33FDDA CRC64;

Query Match 100.0%; Score 1301; DB 1; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-115;  
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAAAPLLLLLLVPPVPLPPLLAQGGGALGNRRHAYVWSSNOHLRREGYTVQVNVNDYLD 60  
 DB 1 MAAAPLLLLLLVPPVPLPPLLAQGGGALGNRRHAYVWSSNOHLRREGYTVQVNVNDYLD 60

OY 61 IYCPHYNSSGVGPGAGPGGGAEOYVLYMVSRNGYRTCNASQGFKRWECNRPAPHSP 120  
 DB 61 IYCPHYNSSGVGPGAGPGGGAEOYVLYMVSRNGYRTCNASQGFKRWECNRPAPHSP 120

OY 121 KFSKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGKPVPT 180  
 DB 121 KFSKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKVFVCCASTSHSGKPVPT 180

OY 181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSTSGTSPKREHPLAVGIAFFLMTFLAS 238  
 DB 181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSTSGTSPKREHPLAVGIAFFLMTFLAS 238

RESULT 2  
 ID EPA3\_MOUSE STANDARD; PRT; 187 AA.  
 AC O08545; O55217;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ephrin-A3 (EPH-related receptor tyrosine kinase ligand 3) (LERK-3)  
 DE (EHK1 ligand) (EHK1-L) (Fragment).  
 GN EFNA3 OR EPLG3 OR LERK3 OR EPL3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=I29;  
 RX MEDLINE=98126446; PubMed=9465306;  
 RA Cerretti D.P., Nelson N.;  
 RT "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),  
 RT mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):  
 RT conservation of intron/exon structure."  
 RL Genomics 47:131-135(1998).  
 RN [2]  
 RP SEQUENCE OF 17-78 FROM N.A.  
 RX MEDLINE=97060319; PubMed=8903354;  
 RA Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;  
 RT "Distinct and overlapping expression patterns of ligands for  
 RT EPH-related receptor tyrosine kinases during mouse embryogenesis."  
 RL Dev. Biol. 179:382-401(1996).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.  
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 CC -----  
 CC EMBL; U92885; AAC39961.1; -;  
 CC EMBL; U90666; AAB50241.1; -;  
 CC MGD; MGI:106644; Efn3.  
 DR InterPro; IPR01799; Ephrin.

DR Pfam; PF00812; Ephrin; 1.  
 DR PRODom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Glycoprotein; GPI-anchor.  
 FT NON\_TER 1 1  
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 19 19 Y -> I (IN REF. 2).  
 FT CONFLICT 33 34 EQ -> DR (IN REF. 2).  
 FT CONFLICT 46 47 RT -> OP (IN REF. 2).  
 FT CONFLICT 78 78 Y -> W (IN REF. 2).  
 SQ SEQUENCE 187 AA: 21171 MW; CCE4915751760743 CRC64;

Query Match 74.0%; Score 963; DB 1; Length 187;  
 Best Local Similarity 91.3%; Pred. No. 1.3e-83;  
 Matches 178; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

OY 44 LRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGAEOYVLYMVSRNGYRTCNASQ 103  
 DB 1 LRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGAEOYVLYMVSRNGYRTCNASQ 52

OY 104 GFKRWECNRPAPHSPKFSKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKV 163  
 DB 53 GSKRWECNRPAPHSPKFSKFORYSAFSLGYEFHAGHEYIYSTPTNHLHWKCLRMKV 112

OY 164 FVCCASTSHSGKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSTSGTSPKREHLP 223  
 DB 113 FVCCASTSHSGKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSTSGTSPKREHLP 172

OY 224 LAVGIAFFLMTFLAS 238  
 DB 173 LAVGIAFFLMTLLAS 187

RESULT 3  
 ID EPA2\_MOUSE STANDARD; PRT; 209 AA.  
 AC P52801;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)  
 DE (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).  
 GN EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SWISS WEBSTER; TISSUE=Brain;  
 RX MEDLINE=95007776; PubMed=7522971;  
 RA Cheng H.J., Flanagan J.G.;  
 RT "Identification and cloning of ELF-1, a developmentally expressed  
 RT ligand for the Wek4 and Sek receptor tyrosine kinases."  
 RL Cell 79:157-168(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95181289; PubMed=7876076;  
 RA Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit V.M.;  
 RT "cDNA cloning and characterization of a Cek7 receptor  
 RT protein-tyrosine kinase ligand that is identical to the ligand  
 RT (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases."  
 RL J. Biol. Chem. 270:3467-3470(1995).  
 CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND  
 CC EPHA5.  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor  
 CC (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.  
 CC -----

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CC -----  
 DR EMBL; U14941; AAA53636.1; -  
 DR EMBL; U14752; AAA68520.1; -  
 DR MGD; MGI:102707; Efn2.  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Glycoprotein; GPI-anchor; Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 209 EPHRIN-A2.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 209 AA; 23586 MW; F1997545F25B9ABC CRC64;

Query Match 33.6%; Score 437; DB 1; Length 209;  
 Best Local Similarity 50.5%; Pred. No. 4.9e-34;  
 Matches 96; Conservative 25; Mismatches 47; Indels 22; Gaps 7;

QY 2 AAAPLLLLLLVPVPLPLLA--QGPGGALGNHAYVWNSNOHLRR-----GYTVQV 53  
 DB 4 AQRPLPLLLL-----LLPLARNEDPARANADRYAVYVWNSRPFQVAVGDDGGGYTVEV 59  
 QY 54 NVNDYLDIYCPHYNSGVGPGGAGGAEQVLYVWNSRNGYRTCNASQ-GFKRWEENR 112  
 DB 60 SINDYLDIYCPHY-----GAPLPAERMEHYLYVWNSGEGHASCCHQRGFKRWEENR 112  
 QY 113 PHAPSPKIFSEKFORYSALSGYEFHAGHEYYIIS-TPTHNLHWKCLRMKVFVCCAS-T 170  
 DB 113 PAAPGGLPKSEKFOQLFTPSGLGFEPFGHEYYIISATPNPLVDRLCLRKVVYRTNET 172  
 QY 171 SHSGEKPVPT 180  
 DB 173 LYEAPEPIFT 182

RESULT 4  
 ID EFA2\_HUMAN STANDARD; PRT; 213 AA.  
 AC O43921; O76020;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)  
 DE (HEK7-6) (HEK7-ligand) (HEK7-L).  
 GN EFA2 OR EPLG6 OR LERK6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98126446; PubMed=9465306;  
 RA Cerretti D.P., Nelson N.;  
 RT "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),  
 mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):  
 conservation of intron/exon structure.";  
 RL Genomics 47:131-135(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Lemerding J.E., McCready P.M., Skowronski E., Adamson A.W.,  
 Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,  
 Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,

RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,  
 RA Tranckheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,  
 RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,  
 RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,  
 RA Carrano A.V.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99045414; PubMed=9826538;  
 RA Aasheim H.C., Pedetour F., Grosgeorge J., Logtenberg T.;  
 RT "Cloning, chromosomal mapping, and tissue expression of the gene  
 encoding the human Eph-family kinase ligand ephrin-A2.";  
 RL Biochem. Biophys. Res. Commun. 252:378-382(1998).  
 CC -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND  
 CC EPHA5  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor  
 CC (POTENTIAL).  
 CC -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.

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CC -----  
 DR EMBL; U92896; AAC39577.1; -  
 DR EMBL; U92893; AAC39577.1; JOINED.  
 DR EMBL; U92894; AAC39577.1; JOINED.  
 DR EMBL; AC004258; AAC04896.1; -  
 DR EMBL; AJ007292; CAA07435.1; -  
 DR MIM; 602756; -  
 DR InterPro; IPR001799; Ephrin.  
 DR Pfam; PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom; PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Glycoprotein; GPI-anchor; Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 213 EPHRIN-A2.  
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 6 6 R -> A (IN REF. 3).  
 FT CONFLICT 25 26 RA -> PP (IN REF. 3).  
 FT CONFLICT 29 30 AA -> RR (IN REF. 3).  
 SQ SEQUENCE 213 AA; 23878 MW; 33C9FBI8168B2D0 CRC64;

Query Match 33.6%; Score 437; DB 1; Length 213;  
 Best Local Similarity 50.5%; Pred. No. 5e-34;  
 Matches 96; Conservative 24; Mismatches 52; Indels 18; Gaps 7;

QY 2 AAAPLL-LLLLVPVPLPLLA--AQGPGGALGNHAYVWNSNOHLRR-----EGTVQV 53  
 DB 4 AQRPLPLLLLPLPPPPFAEAADAARASDRYAVYVWNSRPFHAGAGDDGGGYTVEV 63  
 QY 54 NVNDYLDIYCPHYNSGVGPGGAGGAEQVLYVWNSRNGYRTCNASQ-GFKRWEENR 112  
 DB 64 SINDYLDIYCPHY-----GAPLPAERMEHYLYVWNSGEGHASCCHQRGFKRWEENR 116  
 QY 113 PHAPSPKIFSEKFORYSALSGYEFHAGHEYYIIS-TPTHNLHWKCLRMKVFVCCAS-T 170  
 DB 117 PAAPGGLPKSEKFOQLFTPSGLGFEPFGHEYYIISATPNPLVDRLCLRKVVYRTNET 176  
 QY 171 SHSGEKPVPT 180  
 DB 177 LYEAPEPIFT 186

RESULT 5

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RESULT      6
EFA2_CHICK ID EFA2_CHICK STANDARD; PRT; 200 AA.
AC P52802;
DT DT 01-OCT-1996 (Rel. 34, Created)
DT DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE DE (LERK-6) (ELF-1).
GN EFNA2 OR EPICG6 OR LERK6 OR ELF1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX OX NCBI_TaxID=9031;
RN RN [1]
SEQUENCE FROM N.A.
RX RX MEDLINE=95360981; PubMed=7634327;
RA RA Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.;
RT RT "Complementary gradients in expression and binding of ELF-1 and Mek4
RT RT in development of the topographic retinotectal projection map.";
RL RL Cell 82:371-381(1995)
CC CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EFPA3; EFPA4 AND
CC CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC CC (Potential).
CC CC -1- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS THE TECTUM
CC CC BEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE.
CC CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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-----
CC CC EMBL; L40932; AAC2229.1; .
CC CC InterPro; IPR001799; Ephrin.
CC CC Pfam; PF00812; Ephrin; 1.
CC CC PRINTS; PR01347; EPHRIN.
CC CC ProDom; PD002533; Ephrin; 1.
CC CC PROSITE; PS01299; EPHRIN; 1.
CC CC Glycoprotein; GPI-anchor; Signal.
FT FT SIGNAL 1 22 POTENTIAL.
FT FT CHAIN 23 200 EPHRIN-A2.
FT FT CARBOHYD 36 36 N-LINKED (GLCNAC... ) (POTENTIAL).
FT FT CARBOHYD 161 161 N-LINKED (GLCNAC... ) (POTENTIAL).
FT FT CARBOHYD 175 175 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 200 AA; 23049 MW; 8FAB1AE5EA5EE096 CRC64;
Query Match 32.4%; Score 421; DB 1; Length 200;
Best Local Similarity 47.5%; Pred. No. 1.5e-32;
Matches 86; Conservative 29; Mismatches 50; Indels 16; Gaps 5;

QY 3 AAPLLLLLLVPVPLLPALLAQGGGALGNRHAVYVNSNQHLRRREGTYTVQVNVNDYLDIY 62
   ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 6 AALLAAIVGV-----WSDDPCKVISDRVAVYNRSNPFHRGDYTVVEVSINDYLDIY 60

QY 63 CPHYNSSGVPGAGPGGGAEQVYLVMWSNGVYTCSAQ-GFKRKECHNRPAHPSPK 121
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 CPHYEE-----PLPARMERYVLVMYVNEGASCDHRQKGFKRWECHNRPDSPSPKL 112

QY 122 FSEKFORYSAISLYGEFHAGHEYYIIIS-TPTNHLWKMLRMKVVCASYS-HSGEKPPV 179
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 113 FSEKFQLTFESLGFERPCGHEYYIISASPUNVVDRCLKLKVYVRNTDSLYESPPIF 172

QY 180 T 180
   |

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DR EMBL; U90664; AAB50239.1; -.
DR EMBL; U90665; AAB50240.1; -.
DR MGI; 107444; Efnas.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
KW Alternative splicing.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 228 EPHRIN-A5.
FT CARBOHYD 37 37 N-LINKED (GLCNAC... ) (POTENTIAL).
FT VARSPIC 163 189 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 228 AA; 26339 MW; 85439F5337420022 CRC64;

Query Match 31.9%; Score 414.5; DB 1; Length 228;
Best Local Similarity 39.5%; Pred. No. 7.1e-32;
Matches 98; Conservative 36; Mismatches 67; Indels 47; Gaps 11;

QY 8 LLLLVVPLLLAAGPGG-ALGNHAYVWNSNQHLRREGYTVQVNVNDYLDIYCPHY 66
DB 6 MLTLFLVLMCVFSQDPGSKVADRYAVYWNSSNPRFQGDYHIDVICINDYLDVFCPHY 65
QY 67 NSSGVGPGAGPGGGAEQVYLYMVSRNGYRTC-NASQGFKRWECPNPHAPSPKIFSEK 125
DB 66 EDS-----VPDKTERVLYVWVDFGYSACDHTSGKFKRWECPNPHAPSPKIFSEK 117
QY 126 FQYSAFSLGVEFHAGHYEYIISTP-THNLHWKLCRMKVFV----CCASTSHSGEKPVPPT 180
DB 118 FQFTFSLGFEFPGREYFISSAIPDNGRRSCLKLVFVRPTNSCMKTIGVDRD--- 173
QY 181 LPOFTGPNVKINVLDFE-----GEN-PQVPKLEKISGTSKREHLPLAVGI 228
DB 174 --VFDVNDKVE-NSLEPADDTVHESAPSRGENAAQTPTI-----PSR-----LLAI 217
QY 229 AFLMTFL 236
DB 218 LLFLAML 225

RESULT 9
EFAS_RAT
ID EFA5_RAT STANDARD; PRT; 228 AA.
AC P97605;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE (LERK-7) (AL-1).
GN EFNAS OR EPLG7 OR LERK7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE=95267434; PubMed=7748564;
RA Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong S.C.,
RA Tsai S.P., Goddard A., Henzel W.J., Hefti F., Beck K.D., Caras I.W.;
RT "Cloning of AL-1, a ligand for an Eph-related receptor tyrosine kinase
RT receptor involved in axon bundle formation.";
RL Neuron 14:973-981(1995).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Li Y.Y., McTiernan C.F., Feldman A.M.;
RT "LERK7, rat ligand for Eph-related receptor tyrosine kinase.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
CC INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE

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CC MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS
CC COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF
CC THE FYN TYROSINE KINASE (BY SIMILARITY).
CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
CC EPHB1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
CC IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
CC MICRODOMAINS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, PLACENTA AND LUNG.
CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL; U90664; AAC05801.1; -.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 228 EPHRIN-A5.
FT CARBOHYD 37 37 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 228 AA; 26358 MW; 855985532D580022 CRC64;

Query Match 31.9%; Score 414.5; DB 1; Length 228;
Best Local Similarity 39.5%; Pred. No. 7.1e-32;
Matches 98; Conservative 36; Mismatches 67; Indels 47; Gaps 11;

QY 8 LLLLVVPLLLAAGPGG-ALGNHAYVWNSNQHLRREGYTVQVNVNDYLDIYCPHY 66
DB 6 MLTLFLVLMCVFSQDPGSKVADRYAVYWNSSNPRFQGDYHIDVICINDYLDVFCPHY 65
QY 67 NSSGVGPGAGPGGGAEQVYLYMVSRNGYRTC-NASQGFKRWECPNPHAPSPKIFSEK 125
DB 66 EDS-----VPDKTERVLYVWVDFGYSACDHTSGKFKRWECPNPHAPSPKIFSEK 117
QY 126 FQYSAFSLGVEFHAGHYEYIISTP-THNLHWKLCRMKVFV----CCASTSHSGEKPVPPT 180
DB 118 FQFTFSLGFEFPGREYFISSAIPDNGRRSCLKLVFVRPTNSCMKTIGVDRD--- 173
QY 181 LPOFTGPNVKINVLDFE-----GEN-PQVPKLEKISGTSKREHLPLAVGI 228
DB 174 --VFDVNDKVE-NSLEPADDTVHESAPSRGENAAQTPTI-----PSR-----LLAI 217
QY 229 AFLMTFL 236
DB 218 LLFLAML 225

RESULT 10
EFAS_MOUSE
ID EFA4_MOUSE STANDARD; PRT; 206 AA.
AC O08542; O55218;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin-M4 precursor (EPH-related receptor tyrosine kinase ligand 4)
DE (LERK-4).
GN EFN4 OR EPLG4 OR LERK4 OR EPL4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.

```

RX MEDLINE=97060319; PubMed=8903354;  
 RA Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;  
 RT "Distinct and overlapping expression patterns of ligands for  
 RT Eph-related receptor tyrosine kinases during mouse embryogenesis.";  
 RL Dev. Biol. 179:382-401(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=98126446; PubMed=9465306;  
 RA Cerretti D.P., Nelson N.;  
 RT "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),  
 RT mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):  
 RT conservation of intron/exon structure.";  
 RL Genomics 47:131-135(1998).  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; U90663; AAB50238.1; -  
 DR EMBL; U92890; AAC39962.1; -  
 DR EMBL; U92889; AAC39962.1; JOINED.  
 DR MGD; MGI:106643; Efn4.  
 DR InterPro: IPR001799; Ephrin.  
 DR Pfam: PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom: PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Glycoprotein; GPI-anchor; Signal.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 206 EPHRIN-A4.  
 FT CARBOHYD 33 33 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 98 98 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT SITE 41 43 CELL ATTACHMENT SITE (POTENTIAL).  
 FT CONFLICT 1 4 MRL -> MLLRLGLIYPTRPAPPGLV (IN REF.  
 FT 1).  
 SQ SEQUENCE 206 AA; 22861 MW; 43501971DDIC6EA5 CRC64;

Query Match 31.5%; Score 410; DB 1; Length 206;  
 Best Local Similarity 47.4%; Pred. No. 1.7e-31;  
 Matches 83; Conservative 18; Mismatches 62; Indels 12; Gaps 3;

QY 8 LLLLVVPLLLPALLAOGPGGALGNHRHAYVWNSNQHLLRREGYTVQVNVNDYLDIYCPHYN 67  
 Db 3 LPLLTTLVLAALLGSLRLPGCSLSRLPIYVWNSNPRLRGDAVGLGNDYLDIFCPHYE 62  
 QY 68 SSGVCGPAGPGGGAEQVLYVWNSRNGYRTCA--SQGFKRWECHNRPHAPHSPIKFSK 125  
 Db 63 S-----PGPPEGPETALYVMDWSGYEACTAEGANAFQWNCNMPFAPSVPFSEK 114  
 QY 126 FQYSAFSLGCEYEFHAGHEYIYSTPTTHNLHKLKRMKVFVCC--ASTSHSGKPV 178  
 Db 115 IQRYTFFPLGFEFLPGETYYIYVTPSPGRCRLQVSVCKESGSSHAHPV 169

RESULT 11  
 EFA5\_CHICK  
 ID EFA5\_CHICK STANDARD; PRT; 228 AA.  
 AC P52804;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)  
 DE (LERK-7) (RAGS protein).  
 GN EFNA5 OR RAGS.

OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Posterior tectum;  
 RX MEDLINE=95360980; PubMed=7634326;  
 RA Drescher U., Kremoser C., Handwerker C., Loschinger J., Noda M.,  
 RA Bonhoeffer F.;  
 RT "In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa  
 RT tectal protein related to ligands for Eph receptor tyrosine  
 RT kinases.";  
 RL Cell 82:359-370(1995).  
 CC -!- FUNCTION: INDUCES GROWTH CONE COLLAPSE AND REPULSION OF RETINAL  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor  
 CC (Potential).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A GRADED FASHION ACROSS THE  
 CC TECTUM BEING MORE STRONGLY EXPRESSED TOWARDS THE POSTERIOR POLE.  
 CC -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X90377; CAA62027.1; -  
 DR InterPro: IPR001799; Ephrin.  
 DR Pfam: PF00812; Ephrin; 1.  
 DR PRINTS; PR01347; EPHRIN.  
 DR ProDom: PD002533; Ephrin; 1.  
 DR PROSITE; PS01299; EPHRIN; 1.  
 KW Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 228 EPHRIN-A5.  
 FT CARBOHYD 37 37 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 228 AA; 26206 MW; 56D8E4FBDECF18AD CRC64;

Query Match 31.1%; Score 404.5; DB 1; Length 228;  
 Best Local Similarity 49.1%; Pred. No. 6.2e-31;  
 Matches 79; Conservative 29; Mismatches 42; Indels 11; Gaps 4;

QY 8 LLLLVVPLLLPALLAOGPG-GALGNHRHAYVWNSNQHLLRREGYTVQVNVNDYLDIYCPHY 66  
 Db 6 MLLLAVALWVCVRGQEPGRKAVADRYAVVWNSNPRFQGGDYHDVDCINDYLDVFCPHY 65  
 QY 67 NSGVCGPAGPGGGAEQVLYVWNSRNGYRRC-NASQGFKRWECHNRPHAPHSPIKFSK 125  
 Db 66 EDS-----VPEDKTERIVLYVWVDFGYSDDHTSKGFKRWECHNRPHSPNGPLAFSEK 117  
 QY 126 FQYSAFSLGCEYEFHAGHEYIYSTPTTHNLHKLKRMKVFV 165  
 Db 118 FQLTFFSLGFEFPGREFYFISSAIPDNGRRSCLKLVFV 158

RESULT 12  
 EFA5\_BRARE  
 ID EFA5\_BRARE STANDARD; PRT; 228 AA.  
 AC P79728;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)  
 DE (LERK-7) (AL-1) (ZFEPHL4).  
 GN EFNA5 OR EFNA5B OR ALI OR EPLG7 OR LERK7.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





FT CONFLICT 204 204 S -> T (IN REF. 1).  
SQ SEQUENCE 205 AA; 23802 MW; 5A8F3A6E2091E868 CRC64;

Query Match 28.7%; Score 374; DB 1; Length 205;  
Best Local Similarity 38.7%; Pred. No. 4e-28;  
Matches 86; Conservative 23; Mismatches 87; Indels 26; Gaps 6;  
QY 19 PLLAQGGGALGNRHAYWNSSNOHLRREGYTVQVNVNDYDIYCPHYNSSGVGPGAGPG 78  
Db 7 PLLGLCCSLAAADRHHVFWNSSNPKFREEDYTVHVQLNDYDIICPHYEDDSVADAA--- 63  
QY 79 PGGAEQVLYMVSRNGYRTCN-ASQGKRWECNRPHAPHSPIKFESEKFORYSAFSLGYE 137  
Db 64 ----MERYTLYMVEHQEYVACQPQSKDQVRWNCNRPSAKHGPEKLSKFORFTPFILGKE 119  
QY 138 FHAGHEYYIYSTPTNHLHWCLRNKVFVCCASTSHSGEKPVPPTLPQFTMGPNVKINVLED 197  
Db 120 FKEGHSYYIISKPIYHOESQCLKLKVTV-----NG-----KITHNPQAHVNPQEK 164  
QY 198 -FEGENPQVPKLEKISGTSKPKREHLPLAVGIAFFLMTFLAS 238  
Db 165 RLQADDPVQVLSIGYSAAPRL--FPLVWAVLLPLLLQSQS 204

Search completed: September 28, 2002, 01:48:24  
Job time: 638 sec

Result No.	Query	Score	Query			DB	ID	Description
			Match	Length	Count			
1	Q90YC5	727	55.9	219	13	Q90YC5	Q90YC5 brachydanio	
2	Q923G4	586	45.0	118	11	Q923G4	Q923G4 rattus norv	
3	Q98TZ1	424.5	32.6	202	13	Q98TZ1	Q98TZ1 gallus gall	
4	Q9PTD0	406	31.2	88	13	Q9PTD0	Q9PTD0 ctenophorus	
5	Q9CZS8	406	31.2	206	11	Q9CZS8	Q9CZS8 mus musculus	
6	Q93431	373	28.7	229	13	Q93431	Q93431 brachydanio	
7	Q9D7K8	367	28.2	205	11	Q9D7K8	Q9D7K8 mus musculus	
8	Q9WUE7	338	26.0	102	11	Q9WUE7	Q9WUE7 rattus norv	
9	Q9PTD1	268.5	20.6	93	13	Q9PTD1	Q9PTD1 ctenophorus	
10	Q42304	247.5	19.0	80	11	Q42304	Q42304 brachydanio	
11	Q9CFL3	208	16.0	42	11	Q9CFL3	Q9CFL3 mus musculus	
12	Q90ZG7	178	13.7	70	13	Q90ZG7	Q90ZG7 brachydanio	
13	Q90Z31	166.5	12.8	331	13	Q90Z31	Q90Z31 brachydanio	
14	Q9PT69	164.5	12.6	327	13	Q9PT69	Q9PT69 xenopus lae	
15	Q9PUJ4	162.5	12.5	333	13	Q9PUJ4	Q9PUJ4 gallus gall	
16	Q9V4E1	145	11.1	652	5	Q9V4E1	Q9V4E1 drosophila	





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Q9CZS8
ID Q9CZS8 PRELIMINARY; PRT; 206 AA.
AC Q9CZS8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 10 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:2610529M21, FULL INSERT SEQUENCE.
GN EFNA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adechi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK012195; BAB28092.1; -.
DR MGI; 106643; Efn4.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR PRODOM; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
SQ SEQUENCE 206 AA; 22859 MW; 675E32971D1C6EBC CRC64;

Query Match 31.2%; Score 406; DB 11; Length 206;
Best Local Similarity 46.9%; Pred. No. 3.3e-34;
Matches 82; Conservative 19; Mismatches 62; Indels 12; Gaps 3;

QY 8 LLLLLVPVPLLLAOGPGAGLGNRHAVYVNSSNQHLRREGYTVQVNVNDLYICPHYN 67
DB 3 LPLLTFLVLAALLGSLRPGCSLSRLPIYVNSSNPRLRGDVAVLGFNDYLDIFCPHYE 62
QY 68 SSGVGPAGPGGGGAQVLYVMSRNGYRTCTNA--SQGFKRWECPNRPAPSPKFSK 125
DB 63 S-----PGPEGETALIVDSGYEACTAGANSFORWNCSPAPSPVRFSEK 114
QY 126 FQYSAFSGLGYEHAGHEYYIYSTPHNLHWKRLMKRVVCC--ASTSHSGKPV 178
DB 115 IQRYTFFPLGFLPCLGETYYIISVTPSPGRCRLRLQVSVCKSGSSHSAHPV 169

RESULT 6
ID O93431 PRELIMINARY; PRT; 229 AA.
AC O93431;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EPHRIN A-L1.
OS Brachydanio rerio (zebrafish) (Zebra danio).

Query Match 28.7%; Score 373; DB 13; Length 229;
Best Local Similarity 40.0%; Pred. No. 1e-30;
Matches 84; Conservative 25; Mismatches 59; Indels 42; Gaps 6;

QY 28 ALGNRHAVYVNSSNQHLRREGYTVQVNVNDLYICPHYNSSGVGPGAGPGGGAQYV 87
DB 18 ASAEHSYVYVNSTANFLWDDYTDVDRINDYLDIICPHY-----AHGEIASQEAERV 70
QY 88 LYVMSRNGYRTCTNA--SQGFKRWECPNRPAPSPKFSKFSQYSAFSGLGYEHAGHEYY 146
DB 71 LYVMEVLEDYENCKPHSFDQLRWECSPFPAPHAPEKFSKFSQYSAFSGLGYEHAGHEYY 130
QY 147 ISTPHNLHWKRLMKRVVCCASTSHSGKPVPTLQFTMGPNVKINLVDEGE----- 201
DB 131 ISKPLHHGQECRLKLVGVGPHGSKNKK-----MVKEVELEGKMAAG 176
QY 202 --NP-----QVPKLEKSI--SGTS 216
DB 177 VHNPSNRLPADDPIAMIPVQVRSGSGSVS 206

RESULT 7
ID Q9D7K8 PRELIMINARY; PRT; 205 AA.
AC Q9D7K8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADULT MALE TONGUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:2310004J15, FULL INSERT SEQUENCE.
GN EFNA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adechi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009144; BAB26102.1; -.
DR MGD: MGI:103236; Efnal.
DR InterPro: IPR001799; Ephrin.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00812; Ephrin; 1.
DR PRINTS: PR01347; EPHRIN.
DR PRODOM: PD002533; Ephrin; 1.
DR PROSITE: PS00678; WD_REPEATS.1; UNKNOWN.1.
SQ SEQUENCE 205 AA; 23772 MW; E37E55767459A4EC CRC64;

Query Match 28.2%; Score 367; DB 11; Length 205;
Best Local Similarity 38.3%; Pred. No. 3.7e-30;
Matches 85; Conservative 23; Mismatches 88; Indels 26; Gaps 6;

QY 19 PLLAOGPGGALGNRHAVYWNSSNOHLRREGYTVQVNVNDLYICPHYNSGVGPGAGPG 78
DB 7 PLLGLCCSLAAADRHIVFWNSNPKFREEDYTVHVQLNDLYDICPHYEDDSVADAA--- 63
QY 79 PGGAEOYVLYVMSRNGYRTCN-ASOGFKRWECNRPHAPHSPIKFEKFORYSAFSLGYE 137
DB 64 ----MERYTYLVVHEQYVACQPSKQDOVRWNCNRNSAKHGPKLSVKFORFTFFILGKE 119
QY 138 FHAGHEYYIYSTPTNHLHWKLRMKVFCVCCASTSHSGEKVPVTPQFTMGPNVKINYLE 197
DB 120 FKEGHSYVIYSKPIYHQESQCLKLVTV-----NG-----KITHNPQAHVNPQEK 164
QY 198 -FEGENPQVPKLEKISGTSKREHLPLAVGIAFFLMTFLAS 238
DB 165 RLQADDEVOVLHSGYSAAAPRL--PFLVWVALLPLLLQLQS 204

RESULT 8
Q9WUE7 PRELIMINARY; PRT; 102 AA.
AC Q9WUE7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE EPHRIN A-2 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsunaga T., Davis J.G., Greene M.I.;
RT "Cellular and subcellular compartmentalization of adult peripheral
RT vestibular system by distinctive and overlapping expression of Eph
RT receptors and ephrins.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF131912; AAD33515.1; -.
DR InterPro: IPR001799; Ephrin.
DR Pfam: PF00812; Ephrin; 1.
DR PRODOM: PD002533; Ephrin; 1.
DR PROSITE: PS01299; EPHRIN; 1.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 11838 MW; A497302F7FD7364B CRC64;

Query Match 26.0%; Score 338; DB 11; Length 102;
Best Local Similarity 58.9%; Pred. No. 1.6e-27;
Matches 63; Conservative 13; Mismatches 23; Indels 8; Gaps 2;

QY 49 YTVQVNVNDLYICPHYNSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKR 107

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DB 1 YTVESVNDLYICPHY-----CAPLPAPARMERYILYVMNGEHCASCDHRQRFKR 53
QY 108 WECNRPHAPHSPIKFEKFORYSAFSLGYEFHAGHEYYIYSTPTNHL 154
DB 54 WECNRPAAPGGPLKFEKFOLETFPSLGFEPFGHEYYISATPPNL 100

RESULT 9
Q9PTD1 PRELIMINARY; PRT; 93 AA.
ID Q9PTD1;
AC Q9PTD1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE EPHRIN A2 (FRAGMENT).
OS Ctenophorus ornatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC Ctenophorus.
OX NCBI_TaxID=95347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
RT "Ephrin homologs are expressed in the adult lizard visual system.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF209776; AAF19443.1; -.
DR InterPro: IPR001799; Ephrin.
DR Pfam: PF00812; Ephrin; 1.
DR PRODOM: PD002533; Ephrin; 1.
FT NON_TER 1
FT NON_TER 93
SQ SEQUENCE 93 AA; 11323 MW; BD561F18D34C0F28 CRC64;

Query Match 20.6%; Score 268.5; DB 13; Length 93;
Best Local Similarity 49.5%; Pred. No. 2.4e-20;
Matches 48; Conservative 18; Mismatches 22; Indels 9; Gaps 2;

QY 35 VYWNSSNOHLRREGYTVQVNVNDLYICPHYNSGVGPGAGPGGGAEQYVLYMVSRN 94
DB 1 VFCNRSNPRFWGGEYTVAVSINDYLDYICPYES-----PQPHSRMERYILFVMVNDH 52
QY 95 GYRTG-NASOGFKRWECNRPHAPHSPIKFEKFORYS 130
DB 53 GYLTCHEHMRGFKRWECNRPSQDGLRFESEKFORFT 89

RESULT 10
O42304 PRELIMINARY; PRT; 80 AA.
ID O42304;
AC O42304;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE EPHRIN-A5 (FRAGMENT).
GN EFNA5A.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MacDonald R., Scholes J., Strahle U., Brennan C., Holder N., Brand M.,
RA Wilson S.;
RT "The Pax protein Noi protein is required for commissural axon pathway
RT formation in the rostral forebrain.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y12928; CAA73391.1; -.
DR ZFIN: ZDB-GENE-001128-1; efna5a.
DR InterPro: IPR001799; Ephrin.

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pfam; PF00812; Ephrin; 1.  
DR ProDom; PD002533; Ephrin; 1.  
FT NON\_TER  
NON\_TER 1  
FT 80  
SEQUENCE 80 AA; 9674 MW; 712DDC6058214993 CRC64;

Query Match 19.0%; Score 247.5; DB 13; Length 80;  
Best Local Similarity 51.2%; Pred. No. 3.1e-18;  
Matches 44; Conservative 16; Mismatches 17; Indels 9; Gaps 2;

QY 46 REGTVGVNVNDYLIDVCPHYNSGVCVGPGAGCGGGAEQYLVYWVRNGRYTC-NASQG 104  
Db | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
3 RGDTHDVCINDYLDVYCPIHMDT-----VPEERTERYVLWYNVDGYSCSDHTAKG 54

QY 105 FKRWEKNRPHAPHSPIKFEKFORYS 130  
Db ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
55 FKRWEKNRPHSPNGLFSEKFQLFT 80

RESULT 11  
QCRL3 PRELIMINARY; PRG; 42 AA.

ID QCRL3 AC Q9CRJ3 ID Q9CRJ3 AC Q9CRJ3  
DT 01-JUN-2001 (TEMBLrel. 17, Created)  
CT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)  
DE 12 DAYS EMBRYO EMBRYONIC BODY BETWEEN DIAPHRAM REGION AND NECK CDNA,  
DE RIKEN FULL-LENGTH ENRICED LIBRARY, CLONE:9430025D14, FULL INSERT  
DE SEQUENCE (FRAGMENT).  
GN EFNA3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RC TISSUE=EMBRYONIC BODY BETWEEN DIAPHRAM REGION, AND NECK;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawakura J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aizawa K., Izawa M., Nishio K., Kiyosawa H., Konno H., Adachi J., Fukuda S.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Mikado I., Pesole G., Quackenbush J.,  
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga M., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Humé D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki K., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawasaki H., Kohtsuki S.,  
RA Hayashizaki Y.  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
LR EMBL; AK020438; BAB32100.1;  
DR MGD; MG1:106644; Efna3.  
DR NON\_TER 1  
FT FT  
SQ SEQUENCE 42 AA; 4569 MW; 55DB95E5E0B1B0E2 CRC64;

Query Match 16.0%; Score 208; DB 11; Length 42;  
Best Local Similarity 97.6%; Pred. No. 1.7e-14;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 197 DFGENPQPKLEKSIGSTSPKREHLPLAYGIAPFLMTFLAS 238  
Db ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
1 DFGENPQPKLEKSIGSTSPKREHLPLAYGIAPFLMTFLAS 42

```
Db 12 ILLIFLVDLLGITAT-----NMEDIYNSLNKRFSDDKGYVLYPQIGDRDLICPSSD 64
QY 68 SSGVGCGAGPGGGA--EQVLYMYSR-----NGYRTCNASQGFKRWCNR 112
Db 65 P-----PGPRADYEYKLYLVSSRQADRCVETGAPNLLTCD----- 104
QY 113 PHAPHSPIKSEKQRYSAFSLGYEPHAGHEYIYSTPTNHLNHWKLMKVFVCCASTSH 172
Db 105 --KPNSDMRFTIKFQYSPNLWGHFETKNDHYFIAT--SDGTRQGLSMRGVCAT---- 157
QY 173 SGKPKVPTLPQFTMGPNVK-----INLEDFEGE--NPQVPKLEKSISCTSPKREH 221
Db 158 QGKVVVLKVCQSPYGLPAKSPKPSAGRINPNPNTGNSTHPQIPP-----RGSNGENP 212
QY 222 LP-----LAVGIAFFLM 233
Db 213 LPASNIATVIAAGGSAFLL 233

RESULT 14
Q9PT69 PRELIMINARY; PRT; 327 AA.
AC Q9PT69;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE EPHRIN-B3 PRECOURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RX MEDLINE=20099673; PubMed=10633856;
RA Helbling P.M., Sauter D.M.E., Robinson V., Christiansen J.H.,
RA Wilkinson D.G., Brandli A.W.;
RT "Comparative analysis of embryonic gene expression defines potential
RT interaction sites for Xenopus EphA4 receptors with ephrin-B ligands.";
RL Dev. Dyn. 216:361-373(1999).
DR EMBL; AJ236866; CAB6511.1; -.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 327 AA; 35913 MW; 4B0FA39D4C22DCD CRC64;

Query Match 12.6%; Score 164.5; DB 13; Length 327;
Best Local Similarity 26.6%; Pred. No. 8e-09;
Matches 63; Conservative 31; Mismatches 78; Indels 65; Gaps 13;

QY 35 VYWNSSNOHLR-REGYTVQVNVNDLYCPHYNSSGVGPGAGPGGGAEQVLYMYV-- 91
Db 30 IYWNSSNKRFDTEGYVLVYQIGDRDLICPRSEPQ-----GPFSSSPYKYKLYLVGT 83
QY 92 -----SRNGRYTCNASQGFKRWCNRPHAPHSPIKSEKQRYSAFSLGYEPHAGHEYIY 146
Db 84 KEEMSSCSILRTNLTNL-----LLTCDR---PSODLRTIKFQFSPNLWGHFQSQRDYI 135
QY 147 ISPTNLTNL-----HWKLMKVFVCCASTSHSGEKVPVTLFQFT-----MGPNV 190
Db 136 IATSDGTMGDGIEFTLOGGVCTGKMKVTLKV---GQSPNGATP--PRRPSSAGKDSGISPSV 191
QY 191 KINVLEDFEGENPQVPKLEKSISCTSPKR-----EHLPL-----AVGIAFFLMTF 235
Db 192 -----PNPDIPNVGET--SGNATKTCGNGPLPISHVPLVAGGAAGGALLLLVF 237
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## RESULT 15

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Q9PUJ4 PRELIMINARY; PRT; 333 AA.
AC Q9PUJ4;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE EPHRIN-B2 PRECOURSOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Menzel P., Pasquale E.B.;
RT "Coding sequence of chicken ephrin-B2";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF180729; AAD53948.1; -.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Signal.
FT SIGNAL
FT CHAIN 28 333 EPHRIN-B2.
SQ SEQUENCE 333 AA; 36761 MW; 4C38E8CB211B7783 CRC64;

Query Match 12.5%; Score 162.5; DB 13; Length 333;
Best Local Similarity 27.1%; Pred. No. 1.3e-08;
Matches 61; Conservative 29; Mismatches 92; Indels 43; Gaps 9;

QY 35 VYWNSSN-OHLRREGYTVQVNVNDLYCPHYNSSGVGPGAGPGGGAEQVLYMYVSR 93
Db 35 IYWNSSNPKFLPQGLVLYPQIGDKLDIICPKVDSKTVGQ-----YEYKYVWVKR 85
QY 94 NGYRTCNASQGFKRWCNRP-----HAPHSPIKSEKQRYSAFSLGYEPHAGHEYIYST 149
Db 86 DQADSCAIRKD-----NTPLLCAKPDQDVKFTIKFQFSPNLWGLFQKNDKYVIST 139
QY 150 PTHNLH-----WKCLBMKVFCVCCASTSHSGEKVPVT-----LPQFTMGPNVKINV-- 194
Db 140 SNGSLEGLANQEGGVQCTKTKILMKVQDPNSAGLPRSTDPTKRPEQEAGTNGKSTTS 199
QY 195 --LEDFEGENPQVPKL-EKSISGTSKREHLPLAVGIAFFLMTFL 236
Db 200 PFVKDHSGSSTGSKAGHSILGS-----EVALFAGIASGCIIFI 239
```

Search completed: September 28, 2002, 01:47:36  
Job time: 641 sec



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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 22:47:01 ; Search time 2277.04 Seconds  
(without alignments)  
5844.991 Million cell updates/sec

Title: US-09-904-954-3  
Perfect score: 636  
Sequence: 1 GCCAGACCAACCGACCTC.....TTCTGCGAATTCGTGAGCC 636

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pi.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pi.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
------------	-------	-------	-------	--------	----	-------------

1	636	100.0	636	6	AR001065	AR001065 Sequence	
2	636	100.0	636	6	AR080872	AR080872 Sequence	
3	636	100.0	636	6	AR164470	AR164470 Sequence	
4	636	100.0	636	6	I20810	Sequence 3	
5	636	100.0	636	6	HSU14188	Human recep	
6	636	100.0	1181	9	HSAG352	UJ006352 Homo sapi	
7	497	78.1	1036	9	HSAG353	AJ006353 Homo sapi	
8	419.2	65.9	813	10	MMU90663	U90663 Mus musculus	
9	288.6	45.4	175826	2	AC021890	AC021890 Homo sapi	
10	204.8	32.2	95907	2	AC098750	AC098750 Rattus no	
11	203.2	31.9	3226	10	MM4LK02	U92890 Mus musculus	
c	12	203.2	31.9	289579	2	AC104632	AC104632 Mus muscu
c	13	203.2	31.9	326750	2	AC104327	AC104327 Mus muscu
14	149.8	23.6	981	5	AF317286	AF317286 Gallus ga	
15	121.6	19.1	783	6	AR023765	AR023765 Sequence	
16	120.6	19.0	665	5	CHKELFILIG	L49322 Gallus gall	
17	117.2	18.4	650	10	MM4LK01	U92889 Mus musculus	
18	117.2	18.4	289579	2	AC104632	AC104632 Mus muscu	
19	115.4	18.1	758	9	HUMEF12	L37360 Homo sapien	
20	115.4	18.1	1070	6	AR004292	AR004292 Sequence	
c	21	114.6	18.0	95907	2	AC098750	AC098750 Rattus no
22	112.6	17.7	799	5	GDRNARAGS	X90377 G.domesticu	
23	103.4	16.3	987	9	HSU14187	U14187 Human recep	
24	103.4	16.3	1037	6	AR001064	AR001064 Sequence	
25	103.4	16.3	1037	6	AR080871	AR080871 Sequence	
26	103.4	16.3	1037	6	AR164469	AR164469 Sequence	
27	103.4	16.3	1037	6	I20809	Sequence 1	
28	103.4	16.3	1769	9	BC017722	BC017722 Homo sapi	
29	101.8	16.0	1480	6	AR048795	AR048795 Sequence	
30	101.8	16.0	1480	6	AR103236	AR103236 Sequence	
31	101.8	16.0	1480	6	I56902	Sequence 11	
32	101.8	16.0	1480	6	I88172	Sequence 11	
33	101.8	16.0	1480	9	HUMB61	M57730 Human B61 m	
34	101.8	16.0	1496	6	AX055732	AX055732 Sequence	
35	101.8	16.0	1496	6	AX201360	AX201360 Sequence	
36	101.8	16.0	1498	6	I34756	Sequence 1	
37	101.8	16.0	1498	6	I74360	Sequence 1	
38	100.4	15.8	958	10	MMU26188	U26188 Mus musculus	
39	100.4	15.8	1466	10	BC002046	BC002046 Mus muscu	
40	100.2	15.8	741	10	MMU90662	U90662 Mus musculus	
41	100.2	15.8	1925	9	AK057845	AK057845 Homo sapi	
42	100	15.7	2272	5	DRTKLELF1	Y09668 D.rerio MRN	
43	99	15.6	1650	5	DRTKRAL1	Y09669 D.rerio MRN	
44	98.6	15.5	649	10	MUSMB61B	D38146 Mouse B61 m	
45	97.2	15.3	439	6	AX210445	AX210445 Sequence	

ALIGNMENTS

RESULT	1	636 bp	DNA	linear	PAT 04-DEC-1998
AR001065	AR001065	Sequence 3 from patent US 5738844.			
LOCUS	AR001065	Sequence 3 from patent US 5738844.			
DEFINITION	AR001065	Sequence 3 from patent US 5738844.			
ACCESSION	AR001065	Sequence 3 from patent US 5738844.			
VERSION	AR001065.1	GI:3963132			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 636)				
AUTHORS	Beckmann, M. Patricia, and Cerretti, D. P.				
TITLE	Cytokines that bind the cell surface receptor hek				
JOURNAL	Patent: US 5738844-A 3 14-APR-1998;				
FEATURES	Location/Qualifiers				
source	1..636				
BASE COUNT	102 a	202 c	186 g	146 t	
ORIGIN	/organism="unknown"				

Query Match 100.0%; Score 636; DB 6; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2e-125;

Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GCCAGACAAACCGACCTCGGGGGCGATGCGGCTGCTGCCCTGCTCGGACTGTCTCTC	60						
Db	1	GCCAGACAAACCGACCTCGGGGGCGATGCGGCTGCTGCCCTGCTCGGACTGTCTCTC	60						
Qy	61	TGGGCGGGTTCTTCGCGCTCCCTCTCTGGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC	120						
Db	61	TGGGCGGGTTCTTCGCGCTCCCTCTCTGGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC	120						
Qy	121	TGGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGAGCCCGTGGAGCTGGGGCTCAAC	180						
Db	121	TGGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGAGCCCGTGGTGGAGCTGGGGCTCAAC	180						
Qy	181	GATTACCTAGACATTGCTGCCGCCACTACGAAGGCCAGGGCCCTGAGGGCCCGGAG	240						
Db	181	GATTACCTAGACATTGCTGCCGCCACTACGAAGGCCAGGGCCCTGAGGGCCCGGAG	240						
Qy	241	ACGTTTGCCTTGTACATGTTGGACTGGCCAGGCTATGAGTCTTCCAGGAGAGGGCCCC	300						
Db	241	ACGTTTGCCTTGTACATGTTGGACTGGCCAGGCTATGAGTCTTCCAGGAGAGGGCCCC	300						
Qy	301	CGGGCTACAAAGCGCTGGGTGTCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG	360						
Db	301	CGGGCTACAAAGCGCTGGGTGTCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG	360						
Qy	361	ATTACGGCTTTCACACCTTTCTCCCTCGGCTTTGAGTCTTACCTGGAGAGACTTACTAC	420						
Db	361	ATTACGGCTTTCACACCTTTCTCCCTCGGCTTTGAGTCTTACCTGGAGAGACTTACTAC	420						
Qy	421	TACATCTCGGTGCCACTCCAGAGAGTTCGCGCAGTGTGAGGCTCCAGGTGTCTGTCTC	480						
Db	421	TACATCTCGGTGCCACTCCAGAGAGTTCGCGCAGTGTGAGGCTCCAGGTGTCTGTCTC	480						
Qy	481	TGCTGCAAGGAGAGAGTCTGAGTCAGCCCATCCTCTGTTGGAGCCCTGGAGAGAGTGGC	540						
Db	481	TGCTGCAAGGAGAGAGTCTGAGTCAGCCCATCCTCTGTTGGAGCCCTGGAGAGAGTGGC	540						
Qy	541	ACATCAGGTTGGCGAGGGGGACACTCCAGCCCTCTGCTCTTGCTATTACTGCTG	600						
Db	541	ACATCAGGTTGGCGAGGGGGACACTCCAGCCCTCTGCTCTTGCTATTACTGCTG	600						
Qy	601	CTTCTGATTTCTGCTTCTCGGAATTTCTGTGAGCC	636						
Db	601	CTTCTGATTTCTGCTTCTCGGAATTTCTGTGAGCC	636						
RESULT 2									
LOCUS	AR080872	Sequence 3 from patent US 5969110.		636 bp	DNA	linear	PAT 31-AUG-2000		
DEFINITION	AR080872								
ACCESSION	AR080872								
VERSION	AR080872.1	GI:10007601							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 636)								
AUTHORS	Beckmann,M.Patricia, and Cerretti,D.P.								
TITLE	Antibodies that bind hek ligands								
JOURNAL	Patent: US 5969110-A 3 19-OCT-1999;								
FEATURES	Location/Qualifiers								
source	1..636								
BASE COUNT	102 a	202 c	186 g	146 t					
ORIGIN	/organism="unknown"								
Query Match 100.0%; Score 636; DB 6; Length 636;									
Best Local Similarity 100.0%; Pred. No. 2e-125;									
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GCCAGACAAACCGACCTCGGGGGCGATGCGGCTGCTGCCCTGCTCGGACTGTCTCTC	60						

Db	1	GCAGACAAACCGGACCTCGGGGGGATGCGGCTGCTGCCCTGCTCGGACTGTCCCTC	60																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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DB 601 CTTCTGATTTCTGCTTCTGCGAATTCGTGAGCC 636

RESULT 4
LOCUS I20810 636 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 3 from patent US 5516658.
ACCESSION I20810
VERSION I20810.1 GI:1601165
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 636)
AUTHORS Beckmann,M.Patricia. and Cerretti,D.P.
TITLE DNA encoding cytokines that bind the cell surface receptor hek
JOURNAL US 5516658-A 3 14-MAY-1996;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2e-125;
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DB 61 TGGGCGCGTTCCTCGGCTCCCTCTCGCGGGGCTCCAGCCTCCGACAGTAGTCTAC 120
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RESULT 5
LOCUS HSU14188 636 bp mRNA linear PRI 04-FEB-1995
DEFINITION Human receptor tyrosine kinase LERK-4 (EPLG4) mRNA, complete cds.
ACCESSION U14188
VERSION U14188.1 GI:642834
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 636)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Kozlosky,C.J., Maraskovsky,E., McGrew,J.T., VandenBos,T., Teepe,M., Lyman,S.D., Srinivasan,S., Fletcher,F.A., Gayle,R.B. III, Cerretti,D.P. and Beckmann,M.P.
TITLE Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encoding a family of proteins
JOURNAL Oncogene 10 (2), 299-306 (1995)
MEDLINE 95140419
REFERENCE 2 (bases 1 to 636)
AUTHORS Cerretti,D.P.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1994) Immunex Corp., 51 University St., Seattle, WA 98101, USA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2e-125;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGACCAACCGACCTCGGGGGGATCGCGCTGCTGCCCTGCTGGGACTGTCTC 60
DB 1 GCCAGACCAACCGACCTCGGGGGGATCGCGCTGCTGCCCTGCTGGGACTGTCTC 60
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DB 241 ACCTTTGCTTTGTACATGTTGGACTGGCCAGGCTATGAGTCTGCTGAGGCTCCAGGTGCTGTC 480
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DB 481 TGTGCAAGAGAGAGAGTCTGAGTCAGCCCATCTGTTGGGAGCCCTGGAGAGAGTGGC 540
QY 541 ACATAGGTTGGGAGGGGGACATCCAGCCCTCTGCTCTGCTGCTATGCTGCTG 600
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QY 601 CTCTGATCTTCTGCTTCTGCGAATTCGTGAGCC 636
DB 601 CTCTGATCTTCTGCTTCTGCGAATTCGTGAGCC 636
RESULT 6
LOCUS HSA6352
DEFINITION Homo sapiens mRNA for ephrin-A4 protein, membrane bound form.
ACCESSION AJ006352
VERSION AJ006352.1 GI:3821234
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ephrin-A4 gene.
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1181)
AUTHORS Aasheim,H.C.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-1998) Aasheim H.C., Department of Immunology, The
Norwegian Radium Hospital, Montebello, 0310 n-Oslo, NORWAY
REFERENCE 2 (bases 1 to 1181)
AUTHORS Aasheim,H.C., Munthe,E., Funderud,S., Smeland,E., Beiske,K. and
Logtenberg,T.
TITLE Identification and characterization of a putative secreted splice
variants of the ephrin-A4 (lerk-4) ligand for Eph receptor tyrosine
kinases expressed in cells of the B cell lineage
JOURNAL Unpublished
FEATURES
source
location/Qualifiers
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/clone="pCDM8"
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/note="leukemia"
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BASE COUNT 234 a 353 c 331 g 263 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 GATTACTAGACATTCTGCCCCACTAGAGAGGCCAGGGCCCCCTGAGGCCCCGAG 240
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QY 241 ACCTTTGCTTTGTACATGTTGGACTGGCCAGGCTATGAGTCTGCTGAGGCTCCAGGTGCTGTC 480
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DB 601 CTCTGATCTTCTGCTTCTGCGAATTCGTGAGCC 636
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BASE COUNT 151 a 262 c 225 g 175 t  
ORIGIN

Query Match 65.9%; Score 419.2; DB 10; Length 813;

Best Local Similarity 81.9%; Pred. No. 2.7e-79;

Matches 513; Conservative 0; Mismatches 98; Indels 15; Gaps 2;

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Db 77 CGGGCCGCTGTGTCCTGCTGGGAGTGTCTCTGGGCGCGGCTGCTGGCTCGCGC 136
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Db 137 TGGCGGGTGTCCAGCTCCGCGACCCCACTACTTGGAACTCTCTAACCCAGGTTC 196
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QY 206 ACTFACGAAGGCCAGGCCCCCTGAGGGCCCCGAGAGCTTTGTCTTGTACATGCTGACT 265
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QY 266 GGCAGGCTATGATCTGTCAGGAGAGGCCCCGGGCTTACAGCGCTGGGTGTGCT 325
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Db 317 GGTCAAGCTACGAGGCTGACGCGAGAGGGGCAAAATGCTTCCAGCGCTGGAATGCT 376
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QY 326 CCCTGCCCTTTG-----GCCATGTTCAATTCAGAGAAGATTACGCGTTCCACAC 376
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Db 377 CGATGCTTTTGGCCCTTTCAGCCCTGTTGATTTCTCAGAAAAGATTTCAGCGCTACAC 436
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QY 377 CTCTTCTCCCTGCTTGTAGTTCTTACCTGGAGAGACTTACTACTCATCTCGTGCCCA 436
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Db 437 CTCTCCGCTGGGCTTTGAGTTCTTCCCTGGAGAGACTTACTACTCATCTCGTGCCGA 496
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QY 437 CTCAGAGAGTTCTGCGGCTGCTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGAGAGGA 496
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QY 497 AGTC-----TGAGTCAGCCCTCTGTTGGGAGCCCTGGAGAGTGGACATCAGGTT 550
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 557 GGTATCATCATGATGAGTCACTCTGTTGGAGTCTTGGAGAAAGCGGTACGTCGGGT 616
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RESULT 9  
LOCUS AC021890  
DEFINITION Homo sapiens chromosome 3 clone RP11-498A2, WORKING DRAFT SEQUENCE,  
22 unordered pieces.  
ACCESSION AC021890  
VERSION AC021890.12  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 175826)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C.,  
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Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,  
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Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,  
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,  
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Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
and Gibbs,R.

Direct Submission  
Unpublished  
2 (bases 1 to 175826)  
Worley,K.C.

Direct Submission  
Submitted (22-JAN-2000) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Nov 9, 2000 this sequence version replaced gi:9719697.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: HM2E  
Center clone name: RP11-498A2  
----- Summary Statistics  
Sequencing vector: M13; L08821  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 144734 bases at least Q40  
Consensus quality: 162873 bases at least Q30  
Consensus quality: 169424 bases at least Q20  
Estimated insert size: 170770; sum-of-contigs estimation  
Quality coverage: 0x in Q20 bases; agarose-gel estimation  
Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 22 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 21031: contig of 21031 bp in length

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* 89119 100348: gap of unknown length
* 100349 100448: contig of 11230 bp in length
* 100449 110704: contig of 10256 bp in length
* 110705 110804: gap of unknown length
* 110805 123156: contig of 12352 bp in length
* 123157 123256: gap of unknown length
* 123257 132467: contig of 9211 bp in length
* 132468 132567: gap of unknown length
* 132568 141461: contig of 8894 bp in length
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* 146577 146676: gap of unknown length
* 146677 151201: contig of 4525 bp in length
* 151202 151301: gap of unknown length
* 151302 155722: contig of 4421 bp in length
* 155723 155822: gap of unknown length
* 155823 160148: contig of 4326 bp in length
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* 163025 163124: gap of unknown length
* 163125 165339: contig of 2215 bp in length
* 165340 165439: gap of unknown length
* 165440 168113: contig of 2674 bp in length
* 168114 168213: gap of unknown length
* 168214 169867: contig of 1654 bp in length
* 169868 169967: gap of unknown length
* 169968 171581: contig of 1613 bp in length
* 171581 171680: gap of unknown length
* 171681 172882: contig of 1202 bp in length
* 172883 172982: gap of unknown length
* 172983 174431: contig of 1449 bp in length
* 174432 174531: gap of unknown length
* 174532 175826: contig of 1295 bp in length.
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        /db_xref="taxon:9606"
        /chromosome="3"
        /clone="RP11-498A2"
BASE COUNT 39638 a 46653 c 47059 g 40343 t 2133 others
ORIGIN

Query Match 45.4%; Score 288.6; DB 2; Length 175826;
Best Local Similarity 98.6%; Pred. No. 6.1e-52;
Matches 291; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 138 CAGGTGCTTCGAGGAGCGCGTGGTGGAGCTGGGCTCAACGATTACCTAGACATTTCT 197
Db 115410 CAGGTGCTTCGAGGAGCGCGTGGTGGAGCTGGGCTCAACGATTACCTAGACATTTCT 115469

QY 198 CTGCCCCCACTACGAAGGCCCGCCCGCCCTGAGGGCCCCGAGAGCGTTTGTGTACAT 257
Db 115470 CTGCCCCCACTACGAAGGCCCGCCCGCCCTGAGGGCCCCGAGAGCGTTTGTGTACAT 115529

QY 258 GTGGACTGGCCAGGCTATGAGTCTGCGCAGGCGAGGGCCCCCGGCTACAGCGGTG 317
Db 115530 GTGGACTGGCCAGGCTATGAGTCTGCGCAGGCGAGGGCCCCCGGCTACAGCGGTG 115589

QY 318 GGTGTGCTCCCTGCGCTTTGGCCATGTTCAATTCTCAGAGAAGATTACGCGTTTACACCC 377
Db 115590 GGTGTGCTCCCTGCGCTTTGGCCATGTTCAATTCTCAGAGAAGATTACGCGTTTACACCC 115649

QY 378 TTCTCCCTCGCGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGTG 432

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Db 115650 CTTCTCCCTCGCGCTTTGAGTTCTTACTGGAGAGACTTACTACTACATCTGTGAG 115704

## RESULT 10

AC098750

LOCUS

DEFINITION

AC098750

Rattus norvegicus clone CH230-54E23, \*\*\* SEQUENCING IN PROGRESS

\*\*\*, 50 unordered pieces.

AC098750

AC098750.2 GI:17975664

VERSION

HTG; HTGS\_PHASE1.

KEYWORDS

Norway rat.

SOURCE

ORGANISM

Rattus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 95907)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

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Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,

Washington,S., Williams,G., Williamson,A., Wleczky,R., Wooden,S.,

Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,

Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 95907)

Workley,K.C.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Dec 21, 2001 this sequence version replaced gi:16572779.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GKGA

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Center clone name: CH230-54E23
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 73847 bases at least Q40
Consensus quality: 80027 bases at least Q30
Consensus quality: 84314 bases at least Q20
Estimated insert size: 73738; sum-of-coverage estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.8x in Q20 bases; sum-of-coverage estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Matches 255; Conservative 0; Mismatches 52; Indels 9; Gaps 1;
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DEFINITION	Mus musculus LERK-4 (Epl4) gene, exons 2, 3, 4, and complete cds.		
ACCESSION	U92890		
VERSION	U92890.1	GI:2843101	
KEYWORDS			
SEGMENT	2 of 2		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
AUTHORS	1 (bases 1 to 3226)		
TITLE	Cerretti,D.P. and Nelson,N.		
JOURNAL	Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3), mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6): conservation of intron/exon structure		
MEDLINE	Genomics 47 (1), 131-135 (1998)		
REFERENCE	98126446		
AUTHORS	2 (bases 1 to 3226)		
TITLE	Cerretti,D.P. and Nelson,N.		
JOURNAL	Submitted (11-MAR-1997) Molecular Biology, Immunex Corp., 51 University Street, Seattle, WA 98101, USA		
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\* 21207 23193: contig of 1987 bp in length  
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\* 30819 33823: contig of 3005 bp in length  
\* 33824 33923: gap of unknown length  
\* 33924 35961: contig of 2038 bp in length  
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\* 38733 38832: gap of unknown length  
\* 38833 40937: contig of 2105 bp in length  
\* 40938 41037: gap of unknown length  
\* 41038 43594: contig of 2557 bp in length  
\* 43595 43694: gap of unknown length  
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\* 48084 48183: gap of unknown length  
\* 48184 50630: contig of 2447 bp in length  
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\* 53983 54082: gap of unknown length  
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\* 56168 56267: gap of unknown length  
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ORIGIN

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Best Local Similarity 80.4%; Pred. NO. 8.4e-34;



[illegible]

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RESULT 13
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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SEQUENCE, 66 unordered pieces.
AC104327
AC104327.2 GI:17978117
HTG; HTGS_PHASE1; HTGS_DRAFT.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 326750)
Hua, A. and Roe, B. A.
Mus musculus BAC Clone rp23-295a4
Unpublished
2 (bases 1 to 326750)
Hua, A. and Roe, B. A.
Direct Submission
Submitted (10-DEC-2001) Department of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Dec 24, 2001 this sequence version replaced gi:17439220.

----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 66 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2180: contig of 2180 bp in length
2181 2280: gap of unknown length
2281 4455: contig of 2175 bp in length
4456 4555: gap of unknown length
4556 7347: contig of 2792 bp in length
7348 7447: gap of unknown length
7448 10057: contig of 2610 bp in length
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[illegible]

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QY 394 GAGTTCTTACCTGGAGAGACTTACTACATCTGGTGCCCACTCCAGAGAGTTCTGGC 453
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RESULT 15
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DEFINITION Sequence 3 from patent US 5795734.
ACCESSION AR023765
VERSION AR023765.1 GI:3977059
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 783)
AUTHORS Flanagan,J.G. and Cheng,H.-J.
TITLE EPH receptor ligands, and uses related thereto
JOURNAL Patent: US 5795734-A 3 18-AUG-1998;
FEATURES
Location/Qualifiers
Source 1..783
BASE COUNT 140 a 270 c 232 g 141 t
ORIGIN

Query Match 19.1%; Score 121.6; DB 6; Length 783;
Best Local Similarity 62.0%; Pred. No. 6.2e-16;
Matches 212; Conservative 0; Mismatches 124; Indels 6; Gaps 1;

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QY 165 GGAGCTGGGCTCAACGATTACCTAGACATTTGTCTCCCCCTACTAGAGGGCCAGGGCC 224
Db 232 GGAGGTGAGCATCAATGACTACTCTGGACATCTACTGCCCTCACTACGAGGAGCGCGTGC 291
QY 225 CCTGAGGGCCCGGACACGTTTCTTTGTATGTTGGACTGGCCAGGCTATGATCCTG 284
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Db 472 CCGTCCCGCCACGAGTATTACTACTCTCTGCTCTCCCC 513
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 2002, 00:26:44 ; Search time 239.05 Seconds  
(without alignments)  
4567.905 Million cell updates/sec

Title: US-09-904-954-3

Perfect score: 636

Sequence: 1 GCACACCAAAACCGACCTC.....TTCTGCAATTCGTGAGCC 636

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	636	100.0	636	16	AAQ85888 Human hek-L protei
2	134	21.1	17138	22	AAS14757 Human protease gen
3	121.6	19.1	783	17	AAT15009 Chicken elf-1 cDNA
4	121.6	19.1	783	19	AAV42927 cDNA encoding a a
5	115.4	18.1	1070	16	AAT03883 Eph transmembrane
6	103.4	16.3	1037	16	AAQ85887 Human hek-L protei
7	101.8	16.0	1438	13	AAQ24595 B61 cDNA sequence.
8	101.8	16.0	1480	15	AAQ63770 B61 gene. Homo sa
9	101.8	16.0	1496	22	AAS21387 Human cDNA sequenc

10	101.8	16.0	1496	22	AAQ90574 Human PRO202 CDNA.
11	101.8	16.0	1496	22	AAC91576 Human PRO202 CDNA.
12	101.8	16.0	1527	21	AAC98823 Human pancreatic c
13	97.2	15.3	439	22	AAH81578 Human differential
14	94.8	14.9	1574	23	AAS92779 DNA encoding novel
15	94.8	14.9	1728	17	AAT34292 HEK4 binding prote
16	94.8	14.9	1839	17	AAT18897 Human AL-1 cDNA.
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18	94	14.8	1809	19	AAV42926 cDNA encoding a ma
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20	92	14.5	687	17	AAT32699 Lerk-7 coding sequ
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22	86.2	13.6	555	17	AAT32700 Lerk-6 coding sequ
23	86.2	13.6	555	17	AAAT14009 LERK-6 coding sequ
24	86.2	13.6	555	20	AAAT32761 Murine LERK-6 poly
25	82.2	12.9	314	17	AAT14010 LERK-6 exon. Homo
26	82.2	12.9	314	20	AAAT32766 Exon sequence of h
27	47.6	7.5	3066	23	AAS75651 DNA encoding novel
28	44	6.9	911	21	AAAT76267 Maize glutathione-
29	41.4	6.5	1142	20	AAAT27314 Human secreted pro
30	40.2	6.3	6093	20	AAAT5775 S-erythraea oleand
31	40.2	6.3	50937	21	AAAT09469 Human immune/haema
32	39.8	6.3	424	22	AAAT77253 Streptococcus olea
33	39	6.1	1613	21	AAAT48024 Zea mays DNA fragm
34	38.4	6.0	2271	23	AAS78101 DNA encoding novel
35	37.8	5.9	4403765	22	AAAT99683 Mycobacterium tube
36	36.8	5.8	1618	16	AAAT75423 Human 4-1BB-L poly
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44	36.4	5.7	633	11	AAQ03322 Genomic Eimeria te
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#### ALIGNMENTS

RESULT 1  
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AC AAQ85888;

XX 03-OCT-1995 (first entry)

DT Human hek-L protein cDNA clone C6.

XX Ligand: cell surface; tyrosine kinase receptor; tumorigenesis;  
immunogen; ss.

OS Homo sapiens.

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XX WO9506065-A.

PN 02-MAR-1995.

XX 17-AUG-1994; 94WO-US09282.

XX 20-AUG-1993; 93US-0109745.

XX 30-AUG-1993; 93US-0114426.

XX 03-DEC-1993; 93US-0161132.

PR	09-MAY-1994;	94US-0240124.
XX	(IMMUNEX ) IMMUNEX CORP.	
XX	Beckmann MP, Cerretti DP;	
PI		
XX	WPI; 1995-106811/14.	
DR	P-PSDB; AAR/1482.	
XX		
PT	New isolated DNA encoding hek-L protein or its fusion products -	
PT	useful as assay reagent or for carrying therapeutic and	
PT	diagnostic compounds to leukaemia cells.	
XX		
PS	Claim 3; Page 37; 45pp; English.	
XX		
CC	The sequence is that of a clone encoding hek-L protein, a protein	
CC	that can bind hek (a cell surface receptor tyrosine kinase). Hek-L	
CC	is the first known ligand for hek and can be used to study cellular	
CC	processes regulated by hek (which may be involved in tumorigenesis).	
CC	It is also an immunogen for antibody production, as a reagent for	
CC	detecting hek or hek-L in vitro assays, to determine binding of	
CC	hek proteins, to purify hek proteins, and to carry diagnostic or	
CC	cytotoxic agents to particular leukaemia cells that express the hek	
CC	antigen. Hek-L also binds the elk tyrosine kinase receptors.	
CC	See also AAQ85887.	
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Best Local Similarity 100.0%; Pred. No. 4.1e-154;		
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XX PN  
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XX 25-SEP-2001.  
XX PD  
XX 22-MAR-2001; 2001US-0813819.  
XX PF  
XX 22-MAR-2001; 2001US-0813819.  
XX PR  
XX (APPL-) APPLERA CORP.  
XX PA  
XX WPI: 2001-638014/73.  
XX PI  
XX Merkulov GV, Ye J, Di Francesco V, Beasley EM;  
XX DR  
XX P-PSDB; AAU08749.  
XX XX  
XX New nucleic acids encoding human protease proteins, useful as a major  
XX target for drug action and development, as well as in biological assays  
XX for detecting changes in protease nucleic acid expression  
XX PS  
XX Claim 1: Fig 3; 57pp; English.

CC The invention relates to human protease polypeptides and polynucleotides  
CC which are expressed in the placenta, lung, ovary, colon, kidney, thyroid  
CC gland, prostate, eye and leucocyte. These sequences can be used as models  
CC for the development of human therapeutic targets, in the identification  
CC of therapeutic proteins and serve as targets for the development of drugs  
CC that modulate protease activity in cells and tissues expressing protease.  
CC The nucleic acid molecules are also useful in biological assays for  
CC detecting changes in protease nucleic acid expression and for producing  
CC proteases, which are important for regulating cell proliferation,  
CC differentiation, and signalling processes. This sequence represents  
CC genomic DNA encoding a human protease polypeptide.  
XX  
SQ Sequence 17138 BP; 2315 A; 3492 C; 3363 G; 2751 T; 5217 other;  
  
Query Match 21.1%; Score 134; DB 22; Length 17138;  
Best Local Similarity 80.5%; Pred. No. 1.4e-24;  
Matches 169; Conservative 0; Mismatches 40; Indels 1; Gaps 1;  
  
QY 1 GCCAGACCAACCGGACCTCGGGGCGATGCGGCTCTGCCCCCTGTCGGGACTGTCTTC 60  
Db 16167 gccagaccaaaccgacctcgggcgatgcggtctgccccctgctcggaactgtccta 16226  
QY 61 TGGGCGCGCTTCTCGGCTCCCTCTGCGCGGGGGCTCCAGCTCCGCCACGTAGTCTAC 120  
Db 16227 tgggcccgcg-tctcggctccctctgcgcgggggtccagctccgacgtagtctac 16285  
QY 121 TGAACCTCCAGTAACCCAGTTGCTTCGAGGAGACGCGCTGGTGAGCTGGGCCCTCAAC 180  
Db 16286 tgggaactccagtaacccccaggtagccgggcccagcggcgagcagcaagtctgc 16345  
QY 181 GATTACCTAGACATTGCTGTGCCCCCTACTAC 210  
Db 16346 gcgctcccgggctttgcgcgcgccgccac 16375  
  
RESULT 3  
AAT15009  
ID AAT15009 standard; cDNA; 783 BP.  
XX AC AAT15009;  
XX XX  
XX 02-JUL-1996 (first entry)  
XX DT  
XX Chicken elf-1 cDNA.  
DE DE  
XX Elf-1; EPH receptor ligand; dementia; tachycardia; gene therapy;  
KW diagnosis; transgenic animal; ss; ds.  
XX OS Gallus sp.  
XX XX  
XX Key Location/Qualifiers  
FT 5'UTR 1..85  
FT /tag= a  
FT CDS 86..888  
FT /tag= b  
FT sig\_peptide 86..148  
FT /tag= c  
FT mat\_peptide 149..685  
FT /tag= d  
FT 3'UTR 686..783  
FT /tag= e  
FT polyA\_signal 1471..1476  
FT /tag= f  
XX PN WO9609384-A1.  
XX XX  
XX 28-MAR-1996.  
XX PD  
XX 19-SEP-1995; 95WO-US11869.  
XX PF  
XX 27-FEB-1995; 95US-0393462.  
XX PR  
XX 19-SEP-1994; 94US-0308814.

XX PA (HARD ) HARVARD COLLEGE.  
 XX PI Cheng H, Flanagan JG;  
 XX PI P-PSDB; AAR94767;  
 XX DR WPI; 1996-188446/19.  
 XX DR P-PSDB; AAR94767.  
 XX PT Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis  
 XX PT and treatment of disorders associated with the Elf-1 gene, e.g.  
 XX PT dementia, tachycardia , etc.  
 XX PS Claim 36; Page 87-88; 107pp; English.  
 XX CC A chicken cDNA clone (AAR15009) codes for a novel EPH receptor ligand,  
 XX CC Elf-1 (AAR94766), involved in the formation and maintenance of  
 XX CC ordered spatial arrangements of differentiated tissue. It was  
 XX CC obtd. from a day-3 chick embryo cDNA library using mouse Elf-1  
 XX CC cDNA (see AAR15008) as probe. The cDNA can be used for the prodn.  
 XX CC of recombinant Elf-1, in the breeding of transgenic animals,  
 XX CC for the design of diagnostic probes, and for gene (or antisense)  
 XX CC therapy of cellular and tissue disorders.  
 XX PI Cheng H, Flanagan JG;  
 XX PI P-PSDB; AAR94767;  
 XX PS Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;  
 XX CC

Query Match 19.1%; Score 121.6; DB 17; Length 783;  
 Best Local Similarity 62.0%; Pred. No. 9e-22;  
 Matches 212; Conservative 0; Mismatches 124; Indels 6; Gaps 1;

QY 105 CCGCCAGCTAGTCTACTGGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGACGCCGTGGT 164  
 DB 172 ccgctacgcgtctattggaaccgcagcaacccagggtccaccgcggtgattacaccgt 231  
 QY 165 GGAGCTGGGCTCAACGATTACATGACATTTGCTGCCCCCAGTACGAGGCCAGGGCC 224  
 DB 232 ggaggtgagcatcaatgactacatctggaactctactgacctcactacgagagcgctgc 291  
 QY 225 CCCTGAGGGCCCGAGACGTTTGTGTATGATGGTGGCTGCGCCAGGCTATGAGTCTG 284  
 DB 292 cgcgcgcatgagcgctacgtctctacatggtcaactacgagggccacgcgtcgtg 351  
 QY 285 -----CCAGGAGAGAGGGCCCCCGGCGCTACAAAGCGTGGGTGTGCTCCCTGGCCCTTTGG 338  
 DB 352 cgaccaccgagaggggttcaaacgttgaggatgcaacccgagcgtcccccagcgg 411  
 QY 339 CCATGTTCAATTCTCAGAGAAGATTTCAGCGCTTCACACCTTTCTCCCTCGCTTTGAGTT 398  
 DB 412 accctcaagtctcagagagagttccagctcttcacccccctctctcttcttgggttcgagtt 471  
 QY 399 CTTACCTGGAGAGACTTACTACTACATCTCTCGGTGCCACATCC 440  
 DB 472 ccgtcccgccagagattactacatctctcgtctcccc 513

RESULT 4  
 AAV42927  
 ID AAV42927 standard; cDNA; 783 BP.  
 XX AC AAV42927;  
 XX DT 20-OCT-1998 (first entry)  
 XX DE cDNA encoding an avian Elf-1 protein.  
 XX KW Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP;  
 XX KW tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation;  
 XX KW intracellular signalling; increased; survival; neuronal cell;  
 XX KW neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour;  
 XX KW artificial liver; cartilage; bone formation; ss.  
 XX OS Gallus sp.

FH Key Location/Qualifiers  
 FT 5'UTR 1..85  
 FT /\*tag= a  
 FT CDS 86..688  
 FT /\*tag= b  
 FT /product= Elf-1  
 FT sig\_peptide 86..148  
 FT /\*tag= c  
 FT 3'UTR 686..783  
 FT /\*tag= d  
 XX US5795734-A.  
 PN 18-AUG-1998.  
 XX 31-MAY-1995; 95US-0455001.  
 XX 31-MAY-1995; 95US-0455001.  
 PR 19-SEP-1994; 94US-0308814.  
 PR 27-FEB-1995; 95US-0393462.  
 XX (HARD ) HARVARD COLLEGE.  
 XX Cheng H, Flanagan JG;  
 XX WPI; 1998-466665/40.  
 DR P-PSDB; AAW71007.  
 XX Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor  
 PT - for production of Elf-1 protein, useful for regulating  
 PT proliferation, differentiation, and survival of cells  
 XX Claim 12; Columns 73-76; 53pp; English.  
 XX The present sequence encodes an avian EPH receptor ligand designated  
 CC Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a  
 CC tyrosine kinase ligand, which is linked to the membrane through a  
 CC phosphatidylinositol linkage. It shares some homology to 2 other EPH  
 CC receptor ligands, B61 and LERK-2. The Elf-1 protein modulates  
 CC proliferation, differentiation and survival of EPH receptor-expressing  
 CC cells by stimulating or antagonising intracellular signalling mediated  
 CC by the EPH receptor. Typical of many potential applications are  
 CC increasing survival of neuronal cells in culture (e.g. where intended for  
 CC transplantation), also therapeutically in increase neuron survival  
 CC (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent  
 CC nervous system and lymphatic tumours, to induce differentiation of  
 CC hepatocytes to form an artificial liver, to induce cartilage and bone  
 CC formation.  
 XX Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;  
 SQ

Query Match 19.1%; Score 121.6; DB 19; Length 783;  
 Best Local Similarity 62.0%; Pred. No. 9e-22;  
 Matches 212; Conservative 0; Mismatches 124; Indels 6; Gaps 1;

QY 105 CCGCCAGCTAGTCTACTGGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGACGCCGTGGT 164  
 DB 172 ccgctacgcgtctattggaaccgcagcaacccagggtccaccgcggtgattacaccgt 231  
 QY 165 GGAGCTGGGCTCAACGATTACATGACATTTGCTGCCCCCAGTACGAGGCCAGGGCC 224  
 DB 232 ggaggtgagcatcaatgactacatctggaactctactgacctcactacgagagcgctgc 291  
 QY 225 CCCTGAGGGCCCGAGACGTTTGTGTATGATGGTGGCTGCGCCAGGCTATGAGTCTG 284  
 DB 292 cgcgcgcatgagcgctacgtctctacatggtcaactacgagggccacgcgtcgtg 351  
 QY 285 -----CCAGGAGAGAGGGCCCCCGGCGCTACAAAGCGTGGGTGTGCTCCCTGGCCCTTTGG 338  
 DB 352 cgaccaccgagaggggttcaaacgttgaggatgcaacccgagcgtcccccagcgg 411  
 QY 339 CCATGTTCAATTCTCAGAGAAGATTTCAGCGCTTCACACCTTTCTCCCTCGCTTTGAGTT 398



Db 412 accctcagttctcagagaagttcagctctctcaccctctctcttgggttcagatt 471  
 QY 399 CTTACTCGAGAGACTTACTACTACATCTCGTGCCCACTCC 440  
 Db 472 ccgtcccgccacagagattactactacatctctgctctccccc 513

## RESULT 5

AA03883  
 ID AAT03883 standard; DNA; 1070 BP.  
 XX  
 AC AAT03883;  
 XX  
 DT 16-MAY-1996 (first entry)  
 XX  
 DE Eph transmembrane tyrosine kinase family ligand, Efl-2 encoding DNA.  
 XX  
 KW Efl-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;  
 KW neurological disorder; identification; diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 46..750  
 FT /\*tag= a  
 FT /product= Efl-2  
 XX  
 PN W09527060-A2.  
 XX  
 PD 12-OCT-1995.  
 XX  
 PF 04-APR-1995; 95WO-US04208.  
 XX  
 PR 21-OCT-1994; 94US-0327423.  
 PR 04-APR-1994; 94US-0222075.  
 PR 12-APR-1994; 94US-0229402.  
 PR 01-SEP-1994; 94US-0299567.  
 XX  
 PA (REG-) REGENERON PHARM INC.  
 XX  
 PI Aldrich TH, Davis S, Gale N, Goldfarb M, Maisonnierre PC;  
 PI Yancopoulos GD;  
 XX  
 DR WPI; 1995-358635/46.  
 DR P-PSDB; AAR82605.  
 XX  
 PT Ligands which bind Eph family receptors - used in the diagnosis of  
 PT neurological disorders  
 XX  
 PS Disclosure; Fig 3; 58pp; English.  
 XX  
 CC The DNA encodes an Eph transmembrane tyrosine kinase family ligand  
 CC designated Efl-2. Efl-2 is useful for identifying other ligands for  
 CC EHK-1, -2, -3, Eck and Elk receptors. The ligands are useful in  
 CC promoting a differential function and/or influencing the phenotype,  
 CC such as growth and/or proliferation, of receptor bearing cells. They  
 CC may be used in the diagnosis, and treatment of neurological disorders.  
 XX  
 SQ Sequence 1070 BP; 196 A; 341 C; 334 G; 189 T; 10 other;

Query Match 18.1%; Score 115.4; DB 16; Length 1070;  
 Best Local Similarity 55.6%; Pred. No. 3.9e-20;  
 Matches 271; Conservative 0; Mismatches 201; Indels 15; Gaps 2;

QY 15 GACCTCGGGGCGATCGCGTCTGCCCTGTGGGACTGCTCTGTGGCGCGTCTCT 74  
 Db 48 ggcggcgctcgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 107  
 QY 75 CGGCTCCCTCTGCGCGGGGCTCCAGCTCCGCGACGTAGTCTACTGGAACCTCAGTAA 134  
 Db 108 ggcacaaggcccgaggcgctgggaaacggcatcggtgtactggaacagctccaa 167

QY 135 CCCAGGTTGCTTGCAGGAGACGCCGTGGTGGAGCTGGGCTCAACGATTACCTAGACAT 194  
 Db 168 ccagcacctgcggagagggctacacccgtgcaggtagacgtgaacgactatctgatat 227  
 QY 195 TGTCTGCCCCCACTAC-----GAAGGCCACAGGCCCTTGAGGGCCCCGAGAC 242  
 Db 228 ttactgcccgcactacaacagctcggggcgaggaccgggcccgggagggcgagagca 287  
 QY 243 GTTTGCTTTGTACATGTGGAGTGGCCAGGCTATGAGTCTGCCAGGC---AGAGGGCCC 299  
 Db 288 gtacgtgctacatggtgagccgcaacggtcacccgcaacctgcaacgcccagggctt 347  
 QY 300 CCGGCTTACAAAGCGCTGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAA 359  
 Db 348 caagcgctggagtgcaaccggccgacgccccgcacagccccatcaagtcttcggagaa 407  
 QY 360 GATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTTACCTGGAGAGACTACTA 419  
 Db 408 gtccagcgctacagcgcttctctctggttcacgagttccacgcccgcagagactacta 467  
 QY 420 CTACATCTCGTGCCCACTCCAGAGAGTTCTGGCCAGTGTCTGAGGCTCCAGGTCTCT 479  
 Db 468 ctacatctccagccccactcaacacctgcactggaagtgtctgaggtgagaggttctcgt 527  
 QY 480 CTGCTGC 486  
 Db 528 ctgctgc 534

## RESULT 6

AAQ85887  
 ID AAQ85887 standard; cDNA to mRNA; 1037 BP.  
 XX  
 AC AAQ85887;  
 XX  
 DT 03-OCT-1995 (first entry)  
 XX  
 DE Human hek-L protein cDNA clone A2.  
 XX  
 KW Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;  
 KW immunogen; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 83..799  
 FT /\*tag= a  
 FT sig\_peptide 83..139  
 FT /\*tag= b  
 FT mat\_peptide 140..796  
 FT /\*tag= c  
 XX  
 PN W09506065-A.  
 XX  
 PD 02-MAR-1995.  
 XX  
 PF 17-AUG-1994; 94WO-US09282.  
 XX  
 PR 20-AUG-1993; 93US-0109745.  
 PR 30-AUG-1993; 93US-0114426.  
 PR 03-DEC-1993; 93US-0161132.  
 PR 09-MAY-1994; 94US-0240124.  
 XX  
 PA (IMMV) IMMUNEX CORP.  
 XX  
 PI Beckmann MP, Cerretti DP;  
 XX  
 DR WPI; 1995-106811/14.  
 DR P-PSDB; AAR71481.  
 XX  
 PT New isolated DNA encoding hek-L protein or its fusion products -  
 PT useful as assay reagent or for carrying therapeutic and

PT diagnostic compounds to leukaemia cells.

XX Claim 1; Page 34; 45pp; English.

XX The sequence is that of a clone encoding hek-L protein, a protein  
CC that can bind hek (a cell surface receptor tyrosine kinase). Hek-L  
CC is the first known ligand for hek and can be used to study cellular  
CC processes regulated by hek (which may be involved in tumorigenesis).  
CC It is also an immunogen for antibody production, as a reagent for  
CC detecting hek or hek-L in in vitro assays, to determine binding of  
CC hek proteins, to purify hek proteins, and to carry diagnostic or  
CC cytotoxic agents to particular leukaemia cells that express the hek  
CC antigen. Hek-L also binds the elk tyrosine kinase receptors.  
XX See also AA085888.

XX Sequence 1037 BP; 187 A; 343 C; 337 G; 170 T; 0 other;

Query Match 16.3%; Score 103.4; DB 16; Length 1037;  
Best Local Similarity 54.3%; Pred. No. 4.7e-17;  
Matches 271; Conservative 0; Mismatches 201; Indels 27; Gaps 2;

QY 15 GACCTGGGGGCGATCGCGCTGCTGCCCTGCTGCGGACTGCTCTGGCCCGCTTCT 74  
Db 85 ggcggggctcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 144  
QY 75 CGGCTCCCTCTCGCGGGGGTCCAGCCTCGCCACGCTAGTCTACTGGAATCCAGTAA 134  
Db 145 gccccaaagggcgagggcgctggaaacggcgatcggtgctactggaacagctccaa 204  
QY 135 CCCAGGTGCTTCGAGGAGACGCCGTGTGGAGCTGGGCGCTCAAGATTACCTAGACAT 194  
Db 205 ccagcacctcgcgagaggggtacacccgtgcaggtgaaagtgaacgactatctgatat 264  
QY 195 TGCTCGCCCTACTAGCAAGGC-----CCAGGGCCCTCTGA 230  
Db 265 ttactgcccgcactacaacagctcggggtg9ggcccg9gg9ggcccg9gg9gg 324  
QY 231 GGGCCCCGAGACGCTTTGTTGTACATGGTGGACTGGCCAGGCTATGCTCTGCGAGGC 290  
Db 325 cg9ggcgagagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 384  
QY 291 ---AGAGGCCCCGGGCTCAGAGCGTGGGTGCTCTCCCTGCTTTGGCCATTTCA 347  
Db 385 cagccagggtctcaagctggaggtgcaacggcgccgaccccgccacagcccaatcaa 444  
QY 348 ATTCTCAGAGAATTCAGCGCTTACACGCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407  
Db 445 gtctcggagaaggtccagcgtacagccttctctctctg9gctacgaggtccacgccc 504  
QY 408 AGAGACTTACTACATCTCGGTGCCCCACTCCAGAGAGTTCTGGCCAGTGTGAGGCT 467  
Db 505 ccacgagtagtactacatctccacgcccactcacaacctgcactggaagtgtctgagat 564  
QY 468 CCAGGTGCTGCTGTGTCG 486  
Db 565 gaaggtgtctgctgctgc 583

## RESULT 7

AA024595  
ID AA024595 standard; cDNA to mRNA; 1438 BP.

XX AA024595;

XX DT 06-NOV-1992 (first entry)

XX DE B61 cDNA sequence.

XX KW Early inflammatory response; marker; antibody; therapy; induction;  
XX KW lipopolysaccharides; cytokines; Interleukin-2; IL-2; TNF; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 74..691  
FT /\*tag= a  
FT sig\_peptide 74..128  
FT /\*tag= b  
FT polyA\_signal 1458..1463  
FT /\*tag= c  
XX WO9207094-A.  
XX 30-APR-1992.  
XX 15-OCT-1991; 91WO-US07704.  
XX 16-OCT-1990; 90US-0607741.  
XX (UNMI ) UNIV MICHIGAN.  
XX Dixit VN;  
XX WPI: 1992-167172/20.  
XX P-PSDB; AAR23895.  
XX Gene prod. used as marker to detect inflammatory response - by  
XX detecting the B61 gene in biological fluids or by using  
XX hybridisation probes  
XX Claim 1; Fig 3; 39pp; English.  
XX Poly(A)+ mRNA isolated from human umbilical vein endothelial cells  
CC (HUV) was treated with TNF cyclohexamide and used to construct a  
CC lambda gt11 cDNA library. The library was screened using  
CC radiolabelled cDNA fragments derived from the 5' end of B61 DNA.  
CC Hybridising cDNA inserts were isolated and subcloned into pGEM 7zf  
CC (+) for sequencing. Clone B61.1 contained the entire ORF encoding a  
CC protein of 205 residues (24 kD). The B61 gene is involved in early  
CC inflammatory response and serves as a marker. It may be detected by  
CC probes or by antibody-based immunoassay of biological fluids such as  
CC plasma, CSF or urine. These assays make it possible to predict a  
CC worsening in a disease process and allow the quantitative  
CC assessment of the magnitude of the inflammatory response. This  
CC information will allow the earlier admin. of appropriate therapy,  
CC thereby shortening the disease process and limiting the patient's  
CC exposure to anti-inflammatory/immunosuppressive therapy. B61  
CC induction is rapid and profound, hence it is easily detectable.  
CC The B61 response is highly specific to proinflammatory stimuli,  
CC being only made by cells exposed to lipopolysaccharides or cytokines  
CC such as IL-2 and TNF and not growth factors or interferon.  
XX  
SQ Sequence 1438 BP; 358 A; 412 C; 373 G; 295 T; 0 other;

Query Match 16.0%; Score 101.8; DB 13; Length 1438;  
Best Local Similarity 56.9%; Pred. No. 1.3e-16;  
Matches 253; Conservative 0; Mismatches 177; Indels 15; Gaps 3;

QY 56 TCCTCTGGGCGCGTTCCTCGGCTCCCTCTGGCGGGGGCTCCAGCCTCCGCGACGTAG 115  
Db 81 tctctggggccctctctctggtctgctgcaagtctggtgctgctgctgctgctgctgctg 140  
QY 116 TCTACTGGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGACGCGCTGGAGCTGGGCC 175  
Db 141 tctcttggaacagttccaaatcccaagttccggaatgaggaactacaccatcgtgcagc 200  
QY 176 TCAACGATTACCTAGACATTGCTGCCCGCCACTACCAAGG---CCAGGGCCCCCTGAGG 232  
Db 201 tgaatgactacgtggacatcctgtcccgcactatgaagatcactctgtggcagacgtg 260  
QY 233 GCCCGCAGACGTTGCTTTGTACATGGTGGACTGGCCAGGCTATGATCTCTGCCAGCGAG 292  
Db 261 ccattggagcagatcactctgctggtgagcatgaggaagtagcagctgtgcccagcccc 320

QY 293 AGGGCCCCGGGCTTACAGCGCTGGGTGCTGCTCCCTGCGCTT-----TGGCCATG 343  
 Db 321 ag---tccaaggaccagtcgctgagtcgagtcgacccgcccagtcgacagcatggcccgg 377  
 QY 344 TTCAATTCCTCAGAGAGATTACGCGCTTCACACCTTTCTCCCTCGCGCTTTGAGTCTTAC 403  
 Db 378 agaagtgctgtgagagttccagcgcttcacacctttcaccccttccaccttgggcaaggagttcaag 437  
 QY 404 CTGGAGAGACTTACTACTACTATCATCTCGTGGTCCCACTCCAGAGAGATTCTGCGCCAGTGTCTGA 463  
 Db 438 aaggacacagctactactacatctccaacccatccaccagcatgaagaccgtgcttga 497  
 QY 464 GGCTCCAGGTCTGTCTGCTGCA 488  
 Db 498 ggttgaaggtgactgtcagtgga 522  
 RESULT 8  
 ID AAQ63770 standard; DNA; 1480 BP.  
 AC AAQ63770;  
 DT 10-JAN-1995 (first entry)  
 XX B61 gene.  
 KW eck receptor; eck receptor binding protein; EBP; B61;  
 KW cancer; inflammation; wound; cytokine; protein tyrosine kinase;  
 KW PK; phosphorylation; ds.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 74..691  
 FT CDS /tag- a  
 FT  
 XX  
 PN EP597503-A.  
 XX 18-MAY-1994.  
 XX 15-NOV-1993; 93EP-0118469.  
 XX 13-NOV-1992; 92US-0977708.  
 PR 09-NOV-1993; 93US-0145616.  
 XX (AMGE-) AMGEN INC.  
 PA Bartley TD, Boyle WJ, Fox GM, Parker VP, Welcher AA;  
 PI WPI; 1994-160538/20.  
 XX P-PSDB; AAR53634.  
 DR New eck receptor binding proteins - useful for treating cancer,  
 PT inflammation, wounds, etc.  
 XX  
 PS Disclosure; Page 27-28; 4lpp; English.  
 XX  
 CC The N-terminal sequence of EBP isolated from the conditioned medium  
 CC of the SK-BR-3 cell line was identical to the N-terminal amino acid  
 CC sequence predicted from the expression of the B61 gene (Holzman et al.,  
 CC Mol. Cell Biol. 10, 5830 (1990); WO9207094).  
 CC cDNA encoding EBP having the N-terminal  
 CC NH2-DRHTVFM(N)SSNPKFREDYTHVQ was cloned  
 CC and sequenced and, as expected, found to be identical to the B61 gene.  
 CC The EBP gene expressed in CHO cells resulted in at least two  
 CC polypeptides having different mol. wts. C-terminal sequencing  
 CC revealed only the sequence KRLLA-COOH which indicated a polypeptide  
 CC of 150 amino acids (EBP1-150).  
 XX  
 SQ Sequence 1480 BP; 359 A; 421 C; 393 G; 307 T; 0 other;

Query Match 16.0%; Score 101.8; DB 15; Length 1480;  
 Best Local Similarity 56.9%; Pred. No. 1.3e-16;  
 Matches 253; Conservative 0; Mismatches 177; Indels 15; Gaps 3;  
 QY 56 TCCTCTGGCGCGGTTCCTCGGCTCCCTCTGCGGGGGCTCCAGCCTCCGCCAGGTAG 115  
 Db 81 tctctctgggccccctctcttgggtctgtgtgagtcgtgctgctgctgctgctgctg 140  
 QY 116 TCTACTGGAACCTCCAGTAAACCCAGGTTGCTTCGAGGAGACGCCGCTGSGTGGAGCTGGGCC 175  
 Db 141 tcttctggacagttccaatcccaagttccggaatgagactacaccatcacatgtgcagc 200  
 QY 176 TCAACGATTACCTAGACATGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG 232  
 Db 201 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgtg 260  
 QY 233 GCCCGAGACGTTTGTCTGTACATGGTGGTGGCTGGCCAGGCTATGATCTGCCAGGCAG 292  
 Db 261 ccattgagcagttacatctgtacctgtgtgagcatgaggtaccagctgtgccagcccc 320  
 QY 293 AGGGCCCCGGGCTTACAGCGCTGGGTGCTGCTCCCTGCGCTT-----TGGCCATG 343  
 Db 321 ag---tccaaggaccagtcgctgagtcgacccgcccagtcgacagcatggcccgg 377  
 QY 344 TTCAATTCCTCAGAGAGATTACGCGCTTCACACCTTTCTCCCTCGCGCTTTGAGTCTTAC 403  
 Db 378 agaagtgctgtgagagttccagcgcttcacacctttcaccccttgggcaaggagttcaag 437  
 QY 404 CTGGAGAGACTTACTACTACTATCATCTCGTGGTCCCACTCCAGAGAGATTCTGCGCCAGTGTCTGA 463  
 Db 438 aaggacacagctactactacatctccaacccatccaccagcatgaagaccgtgcttga 497  
 QY 464 GGCTCCAGGTCTGTCTGCTGCA 488  
 Db 498 ggttgaaggtgactgtcagtgga 522  
 RESULT 9  
 ID AAS21387 standard; cDNA; 1496 BP.  
 XX  
 AC AAS21387;  
 DT 24-OCT-2001 (first entry)  
 XX Human cDNA sequence encoding for PRO202 polypeptide.  
 DE Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.  
 XX Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 XX 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US32678.  
 XX  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.



AAC91576;	AC	
XX	AC	
XX	AC	
DT	21-MAR-2001	(first entry)
XX	XX	
XX	XX	
DE	Human PRO202	cdNA.
XX	XX	
KW	Human; PRO;	cytostatic; nootropic; neuroprotective; respiratory general;
KW	antiinflammatory;	antiangiogenic; immunosuppressive; immunostimulant;
KW	PRO agonist;	cancer; inflammatory disorder; immunological disorder; ss.
XX	XX	
OS	Homo sapiens.	

Query Match 16.0%; Score 101.8; DB 22; Length 1496;  
Best Local Similarity 56.9%; Pred. No. 1.3e-16;  
Matches 253: Conservative 0; Mismatches 177; Indels 15; Gaps 3;

	Qy	Db	Qy	Db	Qy	Db
	56	97	116	157	176	217
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QY 123 GAACCTCCAGTAACCCAGGTGCTTCGAGAGAGAGCGCGTGGTGGAGCTGGGCTCAACGA 182  
D 111 111 11111111 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11  
Db 390 gaacagcagcaacccagattccagaggggtgactaccatattgatgtctgtatcaatga 449  
QY 183 TTACTAGACATTGCTGCCCCCACTACGAGGCCAGGCCGCCCTGAGGGCCCCGAGAC 242  
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Db 450 ctacctggatgtttctgacctactatgagagactccgtcccaagaatgagactgagcg 509  
QY 243 GTTTGCTTTGTACATGCTGGAGCTGGCGAGGCTATGACTCTGCGCA-----GCAGAGGG 296  
D 11 11 11111111 111 1111 1111 1111 11 11 11 11 11 11 11 11 11 11 11  
Db 510 ctatgtctctacatggtgaactttgatggtctacagtgctgcagacacttccaaagg 569  
QY 297 CCCCCGGGCTACAAAGCGCTGGGTGCTCCCTGCGCTTTGGCCATGTTCAATTCTCAGA 356  
D 11 11 11 111111 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11  
Db 570 gtccaagagatgggaatgtaaccggcctcactctccaaatggaccgtgaagtctctga 629  
QY 357 GAAGATTACAGCGCTTACACCTTTCTCCCTGCGGCTTTGAGTTCTTACCTGGAGACTTGA 416  
D 11 11 11 111111 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11  
Db 630 aaaattccagctcttcaactccctttctctagatttgaattcaggccagggccgagaata 689  
QY 417 CTACTACATCTCGGTGCGCCACTCCAGAGAGTTCCTGGCCAGTGTCT 460  
D 11111111 11 111111 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11  
Db 690 ttctacatctctctgcaatccagataatggaagaaggtctct 733

RESULT 15  
AAT34292  
ID AAT34292 standard; cdna; 1728 BP.  
XX  
AC AAT34292;  
XX  
XX 24-OCT-1996 (first entry)  
XX  
XX HEK4 binding protein cDNA.  
XX  
XX HEK4 binding protein; HEK4 receptor; EPH-like receptor;  
KW protein tyrosine kinase; ligand; growth; differentiation; cancer;  
KW nervous system disorder; therapy; ss.  
XX  
XX Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 175..861  
FT /\*tag= a  
FT sig\_peptide 175..231  
FT /\*tag= b  
FT mat\_peptide 232..858  
FT /\*tag= c  
XX  
XX WO9623000-A1.  
XX  
XX 01-AUG-1996.  
XX  
XX 16-JAN-1996; 96WO-US01079.  
XX  
XX 27-JAN-1995; 95US-0379802.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Bartley TD, Fox GM;  
XX  
XX WPI; 1996-362633/36.  
DR P-PSDB; AAW00035.  
XX  
XX Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to  
PT modulate growth and differentiation of, e.g. liver and kidney cells,  
PT and to treat cancer and nervous system disorders  
XX  
XX Claim 15; Page 38-39; 65pp; English.  
XX  
XX  
XX A cDNA clone (AAT34292) codes for human HEK4 binding protein (HEK4 BP)  
CC (AAW00035), a protein that binds to and activates HEK4 and ECK

CC receptors. It was isolated from a human placenta cDNA library using  
CC primers (see also AAT34295-96) based on isolated peptides (AAW00036-38)  
CC of HEK4 BP. The cDNA can be used for recombinant prodn. of EPH BP,  
CC useful for modulating the growth and/or differentiation of EPH sub-  
CC family receptor-bearing cells. It can also be used to detect or  
CC quantitate HEK4 BP nucleic acids, to detect abnormalities in the  
CC HEK4 BP gene, or to control expression levels of HEK4 BP.  
XX  
SQ Sequence 1728 BP; 402 A; 495 C; 401 G; 430 T; 0 other;  
  
Query Match 14.9%; Score 94.8; DB 17; Length 1728;  
Best Local Similarity 51.9%; Pred. No. 8.8e-15;  
Matches 241; Conservative 0; Mismatches 217; Indels 6; Gaps 1;  
  
QY 3 CAGACCAAAACCGACCTCGGGGCGATGGGGCTGCTGCCCTCTGCTCGGACTGCTCTCTG 62  
Db 162 ctggccagcggctgattgtcacagtggagatgttgacgtcgtggttctctgctcggat 221  
QY 63 GGCCGGGTTCTCTCGGCTCCCTCTGCGGGGGCTCCAGCCTCCGCCACGTACTCTACTG 122  
Db 222 gtgtgttcaagccaggacccggggtcccaaggccgtcgccgacgcgtactgtctactg 281  
QY 123 GAACCTCCAGTAACCCAGGTGCTTCGAGAGAGCGCGTGGTGGAGCTGGGCTCAACGA 182  
Db 282 gaacagcagcaacccagattccagaggggtgactaccatattgatgtctgtatcaatga 341  
QY 183 TTACTAGACATTGCTGCCCCCACTACGAAGGCCCGAGGCCCTTGGCCATGTTCAATTCTCAGA 242  
Db 342 ctacctggatgtttctgacctactatgaggactccgtcccaagaataaagactgagcg 401  
QY 243 GTTTGCTTTGTACATGCTGGAGCTGGCCAGGCTATGAGTCTCTGCCA-----GGCAGAGGG 296  
Db 402 ctatgtctctacatggtgaactttgatggtacagtgctgcgaccacacttccaaagg 461  
QY 297 CCCCCGGGCTTACAGCGCTGGGTGCTGCCCTGCGCTTTGGCCATGTTCAATTCTCAGA 356  
Db 462 gttcaagagatgggaatgtaaccggcctcactctccaaatggaccgtgaagttctctga 521  
QY 357 GAAGATTACAGCGCTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTGA 416  
Db 522 aaaattccagctcttcaactccctttctctagatttgaattcaggccagggccgagaata 581  
QY 417 CTACTACATCTCGGTGCGCCACTCCAGAGAGTTCCTGGCCAGTGTCT 460  
Db 582 ttctacatctctctgcaatccagataatggaagaaggtctct 625

Search completed: September 28, 2002, 00:26:53  
Job time: 11248 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 22:42:54 ; Search time 65.52 Seconds  
(without alignments)  
2384.355 Million cell updates/sec

Title: US-09-904-954-3  
Perfect score: 636  
Sequence: 1 GCGACGACCAACCGACCTC.....TTCTGCGAATCTGTGAGCC 636

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues  
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	636	100.0	636	1	US-08-240-124-3
2	636	100.0	636	1	US-08-453-943-3
3	636	100.0	636	2	US-09-057-121-3
4	636	100.0	636	4	US-09-358-734-3
5	134	21.1	17138	4	US-09-813-819-3
6	134	21.1	17138	4	US-09-920-048-3
7	121.6	19.1	783	1	US-08-455-001-3
8	121.6	19.1	783	5	PCT-US95-11869-3
9	115.4	18.1	1070	1	US-08-299-567-8
10	103.4	16.3	1037	1	US-08-240-124-1
11	103.4	16.3	1037	1	US-08-453-943-1
12	103.4	16.3	1037	2	US-09-057-121-1
13	103.4	16.3	1037	4	US-09-358-734-1
14	101.8	16.0	1480	1	US-08-448-736-11
15	101.8	16.0	1480	1	US-08-452-779-11
16	101.8	16.0	1480	1	US-08-445-065-11
17	101.8	16.0	1480	3	US-08-959-524-11
18	101.8	16.0	1498	1	US-08-321-162-1
19	101.8	16.0	1498	1	US-08-441-216-1
20	94.8	14.9	1728	3	US-08-379-802-1
21	94.8	14.9	1728	3	US-09-048-129-1
22	94.8	14.9	1728	4	US-09-048-079-1
23	94.8	14.9	1839	1	US-08-442-248-3
24	94.8	14.9	1839	1	US-08-440-815-3
25	94.8	14.9	1839	4	US-08-486-449-3
26	94	14.8	1615	4	US-08-308-814-1
27	94	14.8	1809	1	US-08-455-001-1

28	94	14.8	1809	5	PCT-US95-11869-1	Sequence 1, Appli
29	92	14.5	687	5	PCT-US95-15781-4	Sequence 4, Appli
30	91.6	14.4	642	1	US-09-609-324A-9	Sequence 9, Appli
31	91.6	14.4	642	2	US-08-920-440B-9	Sequence 9, Appli
32	91.6	14.4	642	4	US-09-173-492-9	Sequence 9, Appli
33	91.6	14.4	642	4	US-09-173-133-9	Sequence 9, Appli
34	86.2	13.6	555	1	US-09-609-324A-1	Sequence 1, Appli
35	86.2	13.6	555	2	US-08-920-440B-1	Sequence 1, Appli
36	86.2	13.6	555	4	US-09-173-492-1	Sequence 1, Appli
37	86.2	13.6	555	4	US-09-173-133-1	Sequence 1, Appli
38	86.2	13.6	555	4	US-09-165-533-1	Sequence 1, Appli
39	86.2	13.6	555	5	PCT-US95-12779-1	Sequence 1, Appli
40	86.2	13.6	555	5	PCT-US95-15781-1	Sequence 1, Appli
41	82.2	12.9	314	1	US-09-609-324A-7	Sequence 1, Appli
42	82.2	12.9	314	2	US-08-920-440B-7	Sequence 7, Appli
43	82.2	12.9	314	4	US-09-173-492-7	Sequence 7, Appli
44	82.2	12.9	314	4	US-09-173-133-7	Sequence 7, Appli
45	82.2	12.9	314	4	US-09-165-533-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-08-240-124-3  
; Sequence 3, Application US/08240124  
; Patent No. 5516658  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple system 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240,124  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 636 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: hek-L C6  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 94..630  
; NAME/KEY: CDS  
; LOCATION: 28..633  
; NAME/KEY: sig\_peptide  
; LOCATION: 28..93  
; US-08-240-124-3

Query Match 100.0%; Score 636; DB 1; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2.2e-162;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGACCAACCGGACCTCGGGGGGATCGGCTGCTGCCCTGCTCGGACTGTCCTC 60  
Db 1 GCCAGACCAACCGGACCTCGGGGGGATCGGCTGCTGCCCTGCTCGGACTGTCCTC 60

QY 61 TGGGCGCGTTCCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120  
Db 61 TGGGCGCGTTCCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

QY 121 TGAACCTCCAGTAAACCCAGGTGCTTCGAGGAGACCGCTGTGGAGCTGGGCCCTCAAC 180  
Db 121 TGAACCTCCAGTAAACCCAGGTGCTTCGAGGAGACCGCTGTGGAGCTGGGCCCTCAAC 180

QY 181 GATTACCTAGACATTTCTCCCTCCCTACTAGAGGCCCCAGGGCCCCCTGAGGGCCCCGAG 240  
Db 181 GATTACCTAGACATTTCTCCCTCCCTACTAGAGGCCCCAGGGCCCCCTGAGGGCCCCGAG 240

QY 241 ACGTTTGTCTTGTACATGGTGGAGTGGCCAGGCTATGAGTCTGCCAGGCGAGGGCCCC 300  
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QY 301 CGGCGCTACAGCGCTGGGTGTCTCCCTCCCTTTGGCCATGTTCAATCTCAGAGAAG 360  
Db 301 CGGCGCTACAGCGCTGGGTGTCTCCCTCCCTTTGGCCATGTTCAATCTCAGAGAAG 360

QY 361 ATTCAGCGCTTACACCTTTCTCCCTCGGCTTTGAGTCTTACTCGAGAGACTTACTAC 420  
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RESULT 2  
US-08-453-943-3  
; Sequence 3, Application US/08453943  
; Patent No. 5738844  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE

; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/453,943  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/240,124  
; FILING DATE: 09-MAY-1994  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 636 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: hek-L C6  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 94..630  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 28..633  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 28..93  
; US-08-453-943-3

Query Match 100.0%; Score 636; DB 1; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2.2e-162;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGACCAACCGGACCTCGGGGGGATCGGCTGCTGCCCTGCTCGGACTGTCCTC 60  
Db 1 GCCAGACCAACCGGACCTCGGGGGGATCGGCTGCTGCCCTGCTCGGACTGTCCTC 60

QY 61 TGGGCGCGTTCCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120  
Db 61 TGGGCGCGTTCCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

QY 121 TGAACCTCCAGTAAACCCAGGTGCTTCGAGGAGACCGCTGTGGAGCTGGGCCCTCAAC 180

Db 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGACGCGCTGGTGGAGCTGGGCTCAAC 180  
QY 181 GATTACCTAGACATTTCTGCCCCCAGTACGAGGCCAGGCCCCCTGAGGGCCCCGAG 240  
Db 181 GATTACCTAGACATTTCTGCCCCCAGTACGAGGCCAGGCCCCCTGAGGGCCCCGAG 240  
QY 241 ACCTTTGCTTTTACATGCTGACCTGGGCGGAGGCTATGAGTCTGCGCAGGAGGCCCC 300  
Db 241 ACCTTTGCTTTTACATGCTGACCTGGGCGGAGGCTATGAGTCTGCGCAGGAGGCCCC 300  
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Db 301 CGGGCTTACAAGCGTGGTGTGCTCCCTGCGCTTTGAGTCTTACCTGGAGAGACTTACTAC 420  
QY 361 ATTCAGCGCTTACACACCTTTCTCCCTGCGCTTTGAGTCTTACCTGGAGAGACTTACTAC 480  
Db 361 ATTCAGCGCTTACACACCTTTCTCCCTGCGCTTTGAGTCTTACCTGGAGAGACTTACTAC 480  
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Db 421 TACATCTCGTGGCCCACTCCAGAGAGTCTGGCCAGTCTGAGGCTCCAGGTCTGTGC 480  
QY 481 TCGTCAAGGAGAGGAAGTCTGAGTCAGCCCATCTCTGTTGGAGGCCCTGGAGAGAGTGC 540  
Db 481 TCGTCAAGGAGAGGAAGTCTGAGTCAGCCCATCTCTGTTGGAGGCCCTGGAGAGAGTGC 540  
QY 541 ACATCAGGTCGCGAGGGGGGACACTCCAGCCCTCTGCTCTGCTATTACTGCTG 600  
Db 541 ACATCAGGTCGCGAGGGGGGACACTCCAGCCCTCTGCTCTGCTATTACTGCTG 600  
QY 601 CTTTCGATTCTTCGCTTCTGCGAATTCGTGAGCC 636  
Db 601 CTTTCGATTCTTCGCTTCTGCGAATTCGTGAGCC 636

RESULT 3  
US-09-057-121-3  
; Sequence 3, Application US/09057121  
; Patent No. 5969110  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,121  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/240,124  
; FILING DATE:  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993

ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 636 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: hek-L c6  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 94...630  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 28...633  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 28...93  
US-09-057-121-3  
Query Match 100.0%; Score 636; DB 2; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2.2e-162;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCCAGACCAACCCGACCTCGGGGGGATGCGGGTGTCTCCCTGCTGCGGACTGTCTCTC 60  
Db 1 GCCAGACCAACCCGACCTCGGGGGGATGCGGGTGTCTCCCTGCTGCGGACTGTCTCTC 60  
QY 61 TGGGGCGGCTTCTCGGGTCCCTCTGCGCGGGGCTCCAGCTCCGCCACCTAGTCTAC 120  
Db 61 TGGGGCGGCTTCTCGGGTCCCTCTGCGCGGGGCTCCAGCTCCGCCACCTAGTCTAC 120  
QY 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGAGCGCGTGTGAGCTGGGCTCAAC 180  
Db 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGAGCGCGTGTGAGCTGGGCTCAAC 180  
QY 181 GATTACCTAGACATTTCTGCCCCCACTACGAGGCCAGGGCCCCCTGAGGGCCCCGAG 240  
Db 181 GATTACCTAGACATTTCTGCCCCCACTACGAGGCCAGGGCCCCCTGAGGGCCCCGAG 240  
QY 241 ACCTTTGCTTTTACATGCTGAGCTGGGCTGGCCAGGCTATGAGTCTGCGCAGGAGGCCCC 300  
Db 241 ACCTTTGCTTTTACATGCTGAGCTGGGCTGGCCAGGCTATGAGTCTGCGCAGGAGGCCCC 300  
QY 301 CGGGCTTACAAGCGTGGTGTGCTCCCTGCGCTTTGAGTCTTACCTGGAGAGACTTACTAC 420  
Db 301 CGGGCTTACAAGCGTGGTGTGCTCCCTGCGCTTTGAGTCTTACCTGGAGAGACTTACTAC 420  
QY 361 ATTCAGCGCTTACACACCTTTCTCCCTGCGCTTTGAGTCTTACCTGGAGAGACTTACTAC 480  
Db 361 ATTCAGCGCTTACACACCTTTCTCCCTGCGCTTTGAGTCTTACCTGGAGAGACTTACTAC 480  
QY 421 TACATCTCGTGGCCCACTCCAGAGAGTCTGGCCAGTCTGAGGCTCCAGGTCTGTGC 480  
Db 421 TACATCTCGTGGCCCACTCCAGAGAGTCTGGCCAGTCTGAGGCTCCAGGTCTGTGC 480  
QY 481 TCGTCAAGGAGAGGAAGTCTGAGTCAGCCCATCTCTGTTGGAGGCCCTGGAGAGAGTGC 540  
Db 481 TCGTCAAGGAGAGGAAGTCTGAGTCAGCCCATCTCTGTTGGAGGCCCTGGAGAGAGTGC 540  
QY 541 ACATCAGGTCGCGAGGGGGGACACTCCAGCCCTCTGCTCTGCTATTACTGCTG 600  
Db 541 ACATCAGGTCGCGAGGGGGGACACTCCAGCCCTCTGCTCTGCTATTACTGCTG 600

Db 541 ACATCAGGTGGCGAGGGGGGACACTCCAGCCCCCTCTGTCTCTGTCTATTACTGCTG 600  
QY 601 CTTCGTATTCTCGTCTCTCTCGCAATCTGTGAGCC 636  
Db 601 CTTCGTATTCTCGTCTCTCTCGCAATCTGTGAGCC 636

RESULT 4

US-09-358-734-3  
; Sequence 3, Application US/09358734  
; Patent No. 6274117  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/358,734  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/240,124  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 636 base pairs  
; TYPE: nucleic acid  
; TOPOLOGY: linear  
; STRANDEDNESS: single  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: hek-L C6  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 94..630  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 28..633  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 28..93  
US-09-358-734-3

Query Match 100.0%; Score 636; DB 4; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2.2e-162;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCCAGACCAACCGGACCTCGGGGGCGATCGCGCTCTGCTGCCCTCTGCTGGGACTGTGCTC 60  
Db 1 GCCAGACCAACCGGACCTCGGGGGCGATCGCGCTCTGCTGCCCTCTGCTGGGACTGTGCTC 60  
QY 61 TGGGCGCGCTTCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCGCGCCACGCTAGTCTTAC 120  
Db 61 TGGGCGCGCTTCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCGCGCCACGCTAGTCTTAC 120  
QY 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGTGGGCCCTCAAC 180  
Db 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGTGGGCCCTCAAC 180  
QY 181 GATTACCTAGACATTGCTGCCCCCACTACGAAGGCCAGGGCCCCCTGAGGGCCCCGAG 240  
Db 181 GATTACCTAGACATTGCTGCCCCCACTACGAAGGCCAGGGCCCCCTGAGGGCCCCGAG 240  
QY 241 AGTTTTCGTTTGTACATGGTGACTGGCCAGGCTATGAGTCTCTGCCAGGCAGAGGCCCC 300  
Db 241 AGTTTTCGTTTGTACATGGTGACTGGCCAGGCTATGAGTCTCTGCCAGGCAGAGGCCCC 300  
QY 301 CGGGCCTACAAGCGCTGGGTGTCTCCCTGCCCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360  
Db 301 CGGGCCTACAAGCGCTGGGTGTCTCCCTGCCCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360  
QY 361 ATTCAGCGCTTACACCTTTCTCCCTCGGCTTTGAGTCTTCTTACCTGGAGAGACTTACTAC 420  
Db 361 ATTCAGCGCTTACACCTTTCTCCCTCGGCTTTGAGTCTTCTTACCTGGAGAGACTTACTAC 420  
QY 421 TACATCTCGTGCCCCACTCCAGAGAGTCTTGCCCACTGCTTGAGGCTCCAGGCTGCTGTC 480  
Db 421 TACATCTCGTGCCCCACTCCAGAGAGTCTTGCCCACTGCTTGAGGCTCCAGGCTGCTGTC 480  
QY 481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCTCTGTTGGAGCCCTGGAGAGAGTGCC 540  
Db 481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCTCTGTTGGAGCCCTGGAGAGAGTGCC 540  
QY 541 ACATCAGGTTGGGAGGGGGGACACTCCAGCCCCCTCTGCTCTTGTCTATTACTGCTG 600  
Db 541 ACATCAGGTTGGGAGGGGGGACACTCCAGCCCCCTCTGCTCTTGTCTATTACTGCTG 600  
QY 601 CTTCGTATTCTCGTCTCTCTCGCAATCTGTGAGCC 636  
Db 601 CTTCGTATTCTCGTCTCTCTCGCAATCTGTGAGCC 636

RESULT 5

US-09-813-819-3  
; Sequence 3, Application US/09813819  
; Patent No. 6294368  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV, Gennady et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001177  
; CURRENT APPLICATION NUMBER: US/09/813,819  
; CURRENT FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3:  
; LENGTH: 17138  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(17138)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-813-819-3

Query Match 21.1%; Score 134; DB 4; Length 17138;  
Best Local Similarity 80.5%; Pred. No. 8.9e-27;  
Matches 169; Conservative 0; Mismatches 40; Indels 1; Gaps 1;  
QY 1 GCCAGACCAAAACCGACCTCGGGGGGATGCGGGTGTGCCCCCTGCTGGGAGTGTCTTC 60  
DB 16167 gccagacaaacccgacctcggggcgatgctgctgcccctgctgaggactgtccta 16226  
QY 61 TGGGCGCGTCTCGGCTCCCTCTGCGCGGGGCTCCAGCTCCGCGACGTAGTGTCTAC 120  
DB 16227 tgggcccgcg-tcctcggtccctctcgcgggggctccagctccgcacagtagctctac 16285  
QY 121 TCGAATCCAGTAACCCAGGTGTCTCGAGGAGAGCGCGTGTGGAGCTGGGCGCTCAAC 180  
DB 16286 tggaaactccagtaacccaggtagcggggccgaacccggcgagcgacagccaagtctgc 16345  
QY 181 GATTACCTAGACATGTCTGCCCGCCACTAC 210  
DB 16346 gcgctcccggtttgctgctgcccgcgcac 16375

RESULT 6  
US-09-920-048-3  
; Sequence 3, Application US/09920048  
; Patent No. 6344352  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV, Gennady et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001177DIV  
; CURRENT APPLICATION NUMBER: US/09/920,048  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 09/813,819  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 17138  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(17138)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-920-048-3

Query Match 21.1%; Score 134; DB 4; Length 17138;  
Best Local Similarity 80.5%; Pred. No. 8.9e-27;  
Matches 169; Conservative 0; Mismatches 40; Indels 1; Gaps 1;  
QY 1 GCCAGACCAAAACCGACCTCGGGGGGATGCGGGTGTGCCCCCTGCTGGGAGTGTCTTC 60  
DB 16167 gccagacaaacccgacctcggggcgatgctgctgcccctgctgaggactgtccta 16226  
QY 61 TGGGCGCGTCTCGGCTCCCTCTGCGCGGGGCTCCAGCTCCGCGACGTAGTGTCTAC 120  
DB 16227 tgggcccgcg-tcctcggtccctctcgcgggggctccagctccgcacagtagctctac 16285  
QY 121 TCGAATCCAGTAACCCAGGTGTCTCGAGGAGAGCGCGTGTGGAGCTGGGCGCTCAAC 180  
DB 16286 tggaaactccagtaacccaggtagcggggccgaacccggcgagcgacagccaagtctgc 16345  
QY 181 GATTACCTAGACATGTCTGCCCGCCACTAC 210  
DB 16346 gcgctcccggtttgctgctgcccgcgcac 16375

RESULT 7  
US-08-455-001-3  
; Sequence 3, Application US/08455001

Patent No. 5795734  
; GENERAL INFORMATION:  
; APPLICANT: Flanagan, John G.  
; APPLICANT: Cheng, Hwai-Jong  
; TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related  
; TITLE OF INVENTION: Thereto  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,001  
; FILING DATE: 31 MAY 1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: HMI-011CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 783 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 86..685  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..85  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: 686..783  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 86..148  
US-08-455-001-3

Query Match 19.1%; Score 121.6; DB 1; Length 783;  
Best Local Similarity 62.0%; Pred. No. 7.2e-24;  
Matches 212; Conservative 0; Mismatches 124; Indels 6; Gaps 1;  
QY 105 CGCCACGAGTGTCTACTGGAAGTCCAGTAACCCAGGTTGCTTCGAGGAGAGCGCCGTGT 164  
DB 172 CGCTACGCGGTCTATTGGAACCGGAGCAACCCAGGTTCCACCGCGGGATTACACCT 231  
QY 165 GGAGCTGGGCGCTCAACGATTACCTAGACATTGTCTCCCCCTCACTACGAGGCCAGGGCC 224  
DB 232 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTACGAGGAGCGCGTGC 291  
QY 225 CCCTGAGGCCCGGAGACGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 284  
DB 292 CGCCGAGCGCATGGAGCGCTACGTCCTCTACATGTGTCAACTACGAGGCGCACGCGTCTG 351  
QY 285 -----CCAGGAGAGGGGCGGCGGCGCTACAGCGCTGGGTGTGTGTGTGTGTGTGTGTGT 338  
DB 352 CGACACCGGAGAGAGGCTTCAACAGTTGGGAGTGAACCGCGGCGGCTCCCGGAGCGG 411  
QY 339 CCATGTTCAATTCTCAGAGAAGATTTCAGCGCTTCACACCTTTCTCCCTCGGCTTTTGAGTT 398

Db 412 ACCCTCAAGTTCTCAGAGAAGTTCAGCTCTTCACCCCTTCTCTTGGGCTTCGAGTT 471  
QY 399 CTTACCTGGAGAGACTTACTACTACATCTCGGTGCCACTCC 440  
Db 472 CCGTCCGGCCAGAGTATTACTACATCTCTGCGTCTCCCC 513

RESULT 8  
PCT-US95-11869-3  
; Sequence 3, Application PC/TUS9511869  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related  
; NUMBER OF SEQUENCES: 5  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/11869  
; FILING DATE: 19-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: HMI-011CPPC  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 783 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 86..685  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..85  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: 686..783  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 86..148  
PCT-US95-11869-3

Query Match 19.1%; Score 121.6; DB 5; Length 783;  
Best Local Similarity 62.0%; Pred. No. 7.2e-24;  
Matches 212; Conservative 0; Mismatches 124; Indels 6; Gaps 1;  
QY 105 CCGCCACGAGTCTACTGGAACCTCAGTAACCCAGGTTGCTTCGAGGAGACGCCGTGGT 164  
Db 172 CCGCTACGCGTCTATTGGAACCGGAGAACCCAGGTTCCACCGCGGGGATTACACCGT 231  
QY 165 GGAGCTGGGCTCAACGATTACTAGACATGTGTCGCCCCCACTAGAACGCCAGGGCC 224  
Db 232 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTAGGAGGCGCGTGC 291  
QY 225 CCCTGAGGCGCCGAGACGTTTCTTTGTATGTTGGACTGCCAGGCTATGAGTCCTG 284  
Db 292 CGCCGAGCGCATGGAGCGGTACGCTCTACATGGTCAACTAGAGGGCCACGCGTCCTG 351  
QY 285 -----CCAGGCAGAGGGCCCCCGGCCCTACAAGCGCTGGGTGTGCTCCCTGCGCTTTGG 338  
Db 352 CGACCACCGCAGAGGGCTTCAACGTTGGGAGTGCACCCGCCCGGCTCCCGCAGCGG 411

QY 339 CCATGTTCAATTCACAGAGAAGTTCAGCGCTTCACACCTTTCTCCCTCGGCTTCGAGTT 398  
Db 412 ACCCTCAAGTTCTCAGAGAAGTTCAGCTCTTCACCCCTTCTCTTGGGCTTCGAGTT 471  
QY 399 CTTACCTGGAGAGACTTACTACTACATCTCGGTGCCACTCC 440  
Db 472 CCGTCCGGCCAGAGTATTACTACATCTCTGCGTCTCCCC 513  
RESULT 9  
US-08-299-567-8  
; Sequence 8, Application US/08299567  
; Patent No. 5747033  
; GENERAL INFORMATION:  
; APPLICANT: Davis, et al.  
; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL  
; NUMBER OF SEQUENCES: 8  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,567  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kempier, Gall M.  
; REGISTRATION NUMBER: 32,143  
; REFERENCE/DOCKET NUMBER: REG 290  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 914-345-7400  
; TELEFAX: 914-345-7721  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1070 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-299-567-8

Query Match 18.1%; Score 115.4; DB 1; Length 1070;  
Best Local Similarity 55.6%; Pred. No. 3.7e-22;  
Matches 271; Conservative 0; Mismatches 201; Indels 15; Gaps 2;  
QY 15 GACCTCGGGGCGATCGCGCTGCTGCCCTGCTGCGGACTGTCTCTGGGCCCGCTTCCT 74  
Db 48 GGGCGGCGCTCGCGTCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107  
QY 75 CGGCTCCCTCTCGCGGGGGGCTCCAGCCTCCGCCAGCTAGTCTACTGGAACCTCCAGTAA 134  
Db 108 GGCCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATCGGTGTACTGGAACAGCTCCAA 167  
QY 135 CCCCAGGTTGCTTCGAGGAGAGACCCCGTGGTGGAGCTGGGCTCAACGATTACCTAGACAT 194  
Db 168 CCAGCAGCTTCGCGGAGAGGGCTACACCGTGGAGGTGACGTGAACGACTATCTGATAT 227  
QY 195 TGTCTCCCCCACTAC-----GAAAGCCAGAGGCCCGCCCTGAGGGCCCCGAGAC 242  
Db 228 TTAAGTCCCGCACTACACAGAGCTCGGGGGGCGGACCGGGGCGCGGAGGCGGGCAGACA 287  
QY 243 GTTGTCTTTGTACATGTTGAGCTGCGCAGGCTATGATCTTCCAGGC---AGAGGGCCC 299

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Db 288 GTACGTCTGTATATGGTGGAGCGCAACGGCTACCGCACCTGCAACGGCCAGCGCGGCTT 347
Qy 300 CCGGCGCTACAAGCGCTGGGTGTGCTCCCTGCGCTTTGGCCATGTTCAATTCTCAGAGAA 359
Db 348 CAAGCGCTGGAGTGAACCGCGCGCGCACCGCCGACAGCCCATCAAGTTCTCGAGAA 407
Qy 360 GATTCAGCGCTTACACACCTTCTCCCTCGGCTTTGAGTTCTTTACCTGGAGAGACTTACTA 419
Db 408 GTTCCAGCGCTACAGCGCTTCTCTCTGGCTACGAGTTCCACGCGCGCCACGAGTACTA 467
Qy 420 CTACATCTCGGTGCCACTCGAGAGAGTTCTGGCCAGTGTGAGGCTCCAGGTTGCTGT 479
Db 468 CTATCTCTCCAGCGCCCACTCAACAACCTGCACCTGGAAGTGTCTGAGGATGAAGGTGCT 527
Qy 480 CTGCTGC 486
Db 528 CTGCTGC 534

RESULT 10
US-08-240-124-1
; Sequence 1, Application US/08240124
; Patent No. 5516658
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: CERRETTI, DOUGLAS P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; TITLE OF INVENTION: RECEPTOR HEK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,124
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,132
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/114,426
; FILING DATE: 30-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/109,745
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SEESE, KATHRYN A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2814-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hek-L A2
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FEATURE:
; NAME/KEY: CDS
; LOCATION: 83..799
FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 83..139
FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 140..796
US-08-240-124-1

Query Match 16.3%; Score 103.4; DB 1; Length 1037;
Best Local Similarity 54.3%; Pred. No. 6.2e-19;
Matches 271; Conservative 0; Mismatches 201; Indels 27; Gaps 2;

Qy 15 GACCTCGGGGGGATGCGGCTGCTGCCCTGCTCGGGAGTGTCCCTCTGGCGCGCTTCTCT 74
Db 85 GCGCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 144
Qy 75 CGGCTCCCTCTCTCGCGGGGGCTCCAGCCTCCGCGCACGTAGTCTACTGGAATCCAGTAA 134
Db 145 GCGCCAAAGGGCCCGAGGGGCGCTGGAAACCGGCATGCGGTGTACTGGAACAGCTCCA 204
Qy 135 CCCCAGGTTGCTTCGAGGAGACGCGCTGGTGGAGTGGGCGCTCAACGATTACCTAGACAT 194
Db 205 CCAGCACCTGCGCGGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264
Qy 195 TGTCTGCCCCCACTAGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230
Db 265 TTACTGCGCGCACTACAAAGCTCGGGGGTGGCGCGCGCGGAGACCGGGCGCGGAGG 324
Qy 231 GGGCCCGAGAGACGTTTGTCTTGTACATGTTGGACTGGCCAGGCTATGAGTCTGCGCAGC 290
Db 325 CCGGGCAGAGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
Qy 291 ---AGAGGGCCCCCGGGGCTTACAAGCGCTGCGGTGGTGTGCTCCCTGCGCTTTGGCCATGTTCA 347
Db 385 CAGCCAGGGCTTCAAGCGCTGGAGTGAACCGCGCGCACGCGCCGACAGCCCATCAA 444
Qy 348 ATTCTCAGAGAAGATTCAGCGCTTACACCTTTCCCTCGGCTTTGAGTTTGTACCTGG 407
Db 445 GTTCTCGGAGAAAGTCCAGCGCTTACAGCGCTTCTCTGCGGCTACGAGTTCCAGCGCG 504
Qy 408 AGAGACTTACTACTACTCTCGTCCCACTCCAGAGAGTTCTGGCCAGTGTCTGAGGCT 467
Db 505 CCACGAGTACTACTACTCTCCAGCCCACTCACAACCTGCACCTGGAAGTGTCTGAGGAT 564
Qy 468 CCAGGTGTCTGTCTGCTGC 486
Db 565 GAAGGTGTTGCTGCTGC 583

RESULT 11
US-08-453-943-1
; Sequence 1, Application US/08453943
; Patent No. 5738844
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: CERRETTI, DOUGLAS P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; TITLE OF INVENTION: RECEPTOR HEK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
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; NAME/KEY: CDS
; LOCATION: 83..799
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 83..139
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 140..796
; US-09-057-121-1

Query Match      16.3%; Score 103.4; DB 2; Length 1037;
Best Local Similarity 54.3%; Pred. No. 6.2e-19;
Matches 271; Conservative 0; Mismatches 201; Indels 27; Gaps 2;

QY 15 GACCTCGGGGGGATCGCGCTGCTGCCCTGCTCGGAGCTGCTCTGCGCGCGCTTCCT 74
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Db 85 GCGGGCGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 144
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Db 145 GCGCCAAAGGCGCGGAGGGGCGCTGGGAAACCGGATGCGGTGCTACTGGAACAGCTCCAA 204
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QY 135 CCCAGGTTGCTTCGAGGAGACCGCGTGGAGCTGGGCGCTCAAGCATACCTAGACAT 194
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QY 195 TGTCTGCCCCCACTAGGAAGGC-----CCAGGGCCCCCTGA 230
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Db 265 TTACTGCCCGCACTACAAAGCTCGGGGGTGGGCGGCGGAGACCGGGGCGCGGAGG 324
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QY 231 GGGCCCCGAGAGCTTTGCTTTGCTTGTACATGTTGAGCTGGCCAGGCTATGAGTCTGCCAGGC 290
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QY 291 ----AGAGGGCCCCCGGGGCTTACAGGCTGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 347
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; Sequence 1, Application US/09358734
; Patent No. 6274117
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: CERRETTI, DOUGLAS P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; TITLE OF INVENTION: RECEPTOR HEK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
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; SOFTWARE: Microsoft Word for Apple, Version 5.1a
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; APPLICATION NUMBER: US/09/358,734
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,124
; FILING DATE:
; APPLICATION NUMBER: US 08/114,426
; FILING DATE: 30-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/109,745
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SEESE, KATHRYN A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2814-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hek-L A2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 83..799
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 83..139
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 140..796
; US-09-358-734-1

Query Match      16.3%; Score 103.4; DB 4; Length 1037;
Best Local Similarity 54.3%; Pred. No. 6.2e-19;
Matches 271; Conservative 0; Mismatches 201; Indels 27; Gaps 2;

QY 15 GACCTCGGGGGGATCGCGCTGCTGCCCTGCTGCGGAGCTGCTCTGCGCGCGCTTCCT 74
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Db 85 GCGGGCGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 144
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QY 75 CGGCTCCCTCTCGCGGGGGTCCAGCTCCGCGCACGCTAGTCTACTGGAACCTCCAGTAA 134
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Db 145 GCGCCAAAGGCGCGGAGGGGCGCTGGGAAACCGGATGCGGTGCTACTGGAACAGCTCCAA 204
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QY 135 CCCAGGTTGCTTCGAGGAGACCGCGTGGAGCTGGGCGCTCAAGCATACCTAGACAT 194
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Db 205 CCAGCACCTTCGCGGAGAGGGGTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264
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QY 195 TGTCTGCCCCCACTAGGAAGGC-----CCAGGGCCCCCTGA 230
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Db 265 TTACTGCCCGCACTACAAAGCTCGGGGGTGGGCGGCGGAGACCGGGGCGCGGAGG 324
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QY 231 GGGCCCCGAGAGCTTTGCTTTGCTTGTACATGTTGAGCTGGCCAGGCTATGAGTCTGCCAGGC 290
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QY 291 ----AGAGGGCCCCCGGGGCTTACAGGCTGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 347
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QY 468 CCAGGTGTCTGTCTGTCTGC 486
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RESULT 14
US-08-448-736-11
; Sequence 11, Application US/08448736
; Patent No. 5650504
; GENERAL INFORMATION:
; APPLICANT: Bartley, Timothy Dudley
; APPLICANT: Fox, Gary Michael
; APPLICANT: Boyle, William James
; APPLICANT: Welcher, Andrew Avery
; APPLICANT: Parker, Vann Phillips
; TITLE OF INVENTION: Eck Receptor Ligands
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 Mb
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,736
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,616
; FILING DATE: 09-NOV-1993
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1480 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double-stranded
; TOPOLOGY: linear
US-08-448-736-11

Query Match 16.0%; Score 101.8; DB 1; Length 1480;
Best Local Similarity 56.9%; Pred. No. 1.9e-18;
Matches 253; Conservative 0; Mismatches 177; Indels 15; Gaps 3;

QY 56 TCCTCTGGCGCGGTTCCTCGGCTCCCTCTGCGGGGGCTCCAGGCTCCGCCACGCTAG 115
Db 81 TCCTCTGGGGCCCTCTCTGGGTCTGTGTCAGTCTGGCGGTGTGATCGCCACACCG 140
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Db 141 TCCTCTGGAACAGTTCAAAATCCCAAGTTCGGGAATGAGGACTACACATACATGTGCAGC 200
QY 176 TCAACGATTACCTAGACATTTGTCGCCCCCACTACGAAAG---CCAGGGCCCGCTGAGG 232
Db 201 TGAATGACTACGTGGACATCATCTGTCGCGCACTATGAAGATCACTCTGTGGCAGAGCTG 260
QY 233 GCCCCGAGAGCTTTGCTTTTCTAGCATGGTGACTGGCCAGGCTATGATCTGCTGCCAGCAG 292
Db 261 CCATGGAGCAGTACATACTGTACTCTGTGGAGCATGAGGAGTACCACTGTGCCAGCCCC 320
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QY 293 AGGGCCCCCGGGCTTACAAAGCGCTGGGTGTGTCCTCCCTGGCCCTT-----TGGCCATG 343
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; Sequence 11, Application US/08452779
; Patent No. 5716934
; GENERAL INFORMATION:
; APPLICANT: Bartley, Timothy Dudley
; APPLICANT: Fox, Gary Michael
; APPLICANT: Boyle, William James
; APPLICANT: Welcher, Andrew Avery
; APPLICANT: Parker, Vann Phillips
; TITLE OF INVENTION: Eck Receptor Ligands
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 Mb
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,779
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,616
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1480 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double-stranded
; TOPOLOGY: linear
US-08-452-779-11

Query Match 16.0%; Score 101.8; DB 1; Length 1480;
Best Local Similarity 56.9%; Pred. No. 1.9e-18;
Matches 253; Conservative 0; Mismatches 177; Indels 15; Gaps 3;

QY 56 TCCTCTGGCGCGGTTCCTCGGCTCCCTCTGCGGGGGCTCCAGGCTCCGCCACGCTAG 115
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QY 176 TCAACGATTACCTAGACATTTGCTTTTCTAGCATGGTGACTGGCCAGGCTATGATCTGCTGCCAGCAG 232
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Copyright (c) 1993 - 2000 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	634.4	99.7	1247	25	US-09-652-122-4283
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ALIGNMENTS

RESULT 1  
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; Sequence 3, Application PC/TUS9409282  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/09282  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 636 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: hek-L C6  
FEATURE:

; NAME/KEY: mat\_peptide  
; LOCATION: 94..630  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 28..633  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 28..93  
; PCT-US94-09282-3

Query Match 100.0%; Score 636; DB 1; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2.2e-145;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGACCAACCGGACCTCGGGGGGATCGCGCTGCTGCTGCCCTGCTGCCGACTGTCTC 60  
Db 1 GCCAGACCAACCGGACCTCGGGGGGATCGCGCTGCTGCTGCCCTGCTGCCGACTGTCTC 60  
QY 61 TGGGCGCGGTTCTCTCGGCTCCCTCTCGCGGGGGGTCCAGCCTCCGCCACGCTAGTCTAC 120  
Db 61 TGGGCGCGGTTCTCTCGGCTCCCTCTCGCGGGGGGTCCAGCCTCCGCCACGCTAGTCTAC 120  
QY 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGAGAGCCGCTGTGTGAGCTGGGCTCAAC 180  
Db 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGAGAGCCGCTGTGTGAGCTGGGCTCAAC 180  
QY 181 GATTACTAGACATTTCTGCCCCCACTAGCAAGGCCAGGCCCTGTAGGGCCCCGGAG 240  
Db 181 GATTACTAGACATTTCTGCCCCCACTAGCAAGGCCAGGCCCTGTAGGGCCCCGGAG 240  
QY 241 ACCTTTGCTTTGTACATGTTGGACTGGCCAGGCTATGAGTCTGCCAGGAGAGGCC 300  
Db 241 ACCTTTGCTTTGTACATGTTGGACTGGCCAGGCTATGAGTCTGCCAGGAGAGGCC 300  
QY 301 CGGGCCTACAAGCGCTGGGTGCTGCTCCCTGCTCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360  
Db 301 CGGGCCTACAAGCGCTGGGTGCTGCTCCCTGCTCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360  
QY 361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTCTTACCTGGAGAGACTTACTAC 420  
Db 361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTCTTACCTGGAGAGACTTACTAC 420  
QY 421 TACATCTCGGTGCCCACTCCAGAGATTCTGCCAGTGTGTCAGGCTCCAGGTGCTGTCT 480  
Db 421 TACATCTCGGTGCCCACTCCAGAGATTCTGCCAGTGTGTCAGGCTCCAGGTGCTGTCT 480  
QY 481 TGCTGCAAGGAGAGAGAGTCTGAGTCAGCCCATCTCTGTTGGAGCCCTGGAGAGAGTGGC 540  
Db 481 TGCTGCAAGGAGAGAGAGTCTGAGTCAGCCCATCTCTGTTGGAGCCCTGGAGAGAGTGGC 540  
QY 541 ACATCAGGTTGGGAGGGGGGACACTCCAGGCCCTCTGCTCTGCTTGTCTATTACTGCTG 600  
Db 541 ACATCAGGTTGGGAGGGGGGACACTCCAGGCCCTCTGCTCTGCTTGTCTATTACTGCTG 600  
QY 601 CTCTGATTTCTCGTCTTCTTCGGAATTCCTGTGAGCC 636  
Db 601 CTCTGATTTCTCGTCTTCTTCGGAATTCCTGTGAGCC 636

RESULT 2  
US-08-161-132-3  
; Sequence 3, Application US/08161132  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE

STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/161,132  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/114,426  
FILING DATE: 30-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/109,745  
FILING DATE: 20-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: SEESE, KATHRYN A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2814-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 636 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: hek-L C6  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 94...630  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 28...633  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 28...93  
US-08-161-132-3

Query Match 100.0%; Score 636; DB 5; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2.2e-145;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACAGACAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCTGCTCGGAGCTGTCCTC 60  
DB 1 GCACAGACAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCTGCTCGGAGCTGTCCTC 60

QY 61 TGGGCGCGCTTCTCGGCTCCCTCTGCGCGGGGGCTCCAGCTCCGCGACCTAGTCTAC 120  
DB 61 TGGGCGCGCTTCTCGGCTCCCTCTGCGCGGGGGCTCCAGCTCCGCGACCTAGTCTAC 120

QY 121 TGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGAGCGCGTGGTGGAGCTGGGCGCTCAAC 180  
DB 121 TGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGAGCGCGTGGTGGAGCTGGGCGCTCAAC 180

QY 181 GATTACCTAGACATTGCTGCCCGCCACTACGAAGGCCCGGCGCCCTCGAGGGCCCCGAG 240  
DB 181 GATTACCTAGACATTGCTGCCCGCCACTACGAAGGCCCGGCGCCCTCGAGGGCCCCGAG 240

QY 241 ACGTTTGTCTTTGTACATGTTGGACTGGCCAGGCTATGAGTCTCTGCGAGGAGGCCCC 300  
DB 241 ACGTTTGTCTTTGTACATGTTGGACTGGCCAGGCTATGAGTCTCTGCGAGGAGGCCCC 300

QY 301 CGGGCCTAACAGCGCTGGGTGTCTCCCTGCGCCCTTTGGCCATGTTCAATTCAGAGAAG 360  
DB 301 CGGGCCTAACAGCGCTGGGTGTCTCCCTGCGCCCTTTGGCCATGTTCAATTCAGAGAAG 360

QY 361 ATTACAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTCTTACCTGGAGAGACTTACTAC 420  
DB 361 ATTACAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTCTTACCTGGAGAGACTTACTAC 420

QY 421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGTCTGAGGCTCCAGGTGTCTGTC 480  
DB 421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGTCTGAGGCTCCAGGTGTCTGTC 480

QY 481 TGCTCAAGAGAGAGAAAGTCTGAGTACGCCCATCTCTGTTGGAGCGCTCGAGAGAGTGC 540  
DB 481 TGCTCAAGAGAGAGAAAGTCTGAGTACGCCCATCTCTGTTGGAGCGCTCGAGAGAGTGC 540

QY 541 ACATCAGGTGGCGAGGGGGGACACTCCAGCGCCCTCTGCTCTGTTGCTATTACTGCTG 600  
DB 541 ACATCAGGTGGCGAGGGGGGACACTCCAGCGCCCTCTGCTCTGTTGCTATTACTGCTG 600

QY 601 CTTCTGATTCTTCGTCTTCTGCGAAATTCGTGTGAGCC 636  
DB 601 CTTCTGATTCTTCGTCTTCTGCGAAATTCGTGTGAGCC 636

RESULT 3  
US-09-440-302A-839  
; Sequence 839, Application US/09440302A  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Lukashev, Matvey E.  
; TITLE OF INVENTION: Human Neurobiology Array  
; FILE REFERENCE: CLON-006CIP11  
; CURRENT APPLICATION NUMBER: US/09/440,302A  
; CURRENT FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 1193  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 839  
; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-440-302A-839

Query Match 100.0%; Score 636; DB 18; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2.2e-145;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACAGACAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCTGCTCGGAGCTGTCCTC 60  
DB 1 GCACAGACAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCTGCTCGGAGCTGTCCTC 60

QY 61 TGGGCGCGCTTCTCGGCTCCCTCTGCGCGGGGGCTCCAGCTCCGCGACCTAGTCTAC 120  
DB 61 TGGGCGCGCTTCTCGGCTCCCTCTGCGCGGGGGCTCCAGCTCCGCGACCTAGTCTAC 120

QY 121 TGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGAGCGCGTGGTGGAGCTGGGCGCTCAAC 180  
DB 121 TGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGAGCGCGTGGTGGAGCTGGGCGCTCAAC 180

QY 181 GATTACCTAGACATTGCTGCCCGCCACTACGAAGGCCCGGCGCCCTCGAGGGCCCCGAG 240  
DB 181 GATTACCTAGACATTGCTGCCCGCCACTACGAAGGCCCGGCGCCCTCGAGGGCCCCGAG 240

QY 241 ACGTTTGTCTTTGTACATGTTGGACTGGCCAGGCTATGAGTCTCTGCGAGGAGGCCCC 300  
DB 241 ACGTTTGTCTTTGTACATGTTGGACTGGCCAGGCTATGAGTCTCTGCGAGGAGGCCCC 300

QY 301 CGGGCCTAACAGCGCTGGGTGTCTCCCTGCGCCCTTTGGCCATGTTCAATTCAGAGAAG 360  
DB 301 CGGGCCTAACAGCGCTGGGTGTCTCCCTGCGCCCTTTGGCCATGTTCAATTCAGAGAAG 360

QY 361 ATTACGCGCTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420  
Db 361 attcagcgcttcaacacctttctccctcggtttgagttcttactctgagagacttactac 420  
QY 421 TACATCTCGGTGCCACTCCAGAGAGTTTCGGCCAGTGTGAGGCTCCAGGTGCTGTGTC 480  
Db 421 tacatctcggtgccactccagagagtttcggccagtgtgaggtccaggtgtctgtc 480  
QY 481 TGTCTGAAGGAGAGAGTGTGAGTCAAGCCATCTCTTGGGAGCCCTGGAGAGAGTGGC 540  
Db 481 tgtctgaaggagagagagtgtagtcaagccatctcttgggagccctggagagagtgc 540  
QY 541 ACATCAGGTGGCGAGGGGGGACACTCCAGCCGCCCTCTCTCTTGTCTTACTGCTG 600  
Db 541 acatcaggtggcgaggggggacactccagccgccctctctcttgtcttactgctg 600  
QY 601 CTCTGATTTCTTCTGCTTCTGCGAATTTCTGTGAGCC 636  
Db 601 ctctgatttcttctgcttctgcgaaattctgtgagcc 636

RESULT 4  
US-09-904-954-3  
; Sequence 3, Application US/09904954  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; CERRETI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/904,954  
; FILING DATE: 12-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/240,124  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SESEE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 636 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: hek-L C6

FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 94..630  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 28..633  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 28..93  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-904-954-3  
Query Match 100.0%; Score 636; DB 34; Length 636;  
Best Local Similarity 100.0%; Pred. No. 2.2e-145;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCCAGACCAACCGGACCTCGGGGGGATCGGGCTGCTGCCCTGTGCGGAGTGTCTC 60  
Db 1 GCCAGACCAACCGGACCTCGGGGGGATCGGGCTGCTGCCCTGTGCGGAGTGTCTC 60  
QY 61 TGGGCGCGCTTCTCGGCTCCCTCTGCGGGGGGCTCCAGCTCCGCCACGCTAGTCTAC 120  
Db 61 TGGGCGCGCTTCTCGGCTCCCTCTGCGGGGGGCTCCAGCTCCGCCACGCTAGTCTAC 120  
QY 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCTCAAC 180  
Db 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGAGAGCCGCTGGTGGAGCTGGGCTCAAC 180  
QY 181 GATTACCTAGACATTTGCTGCCCTCCACTAGAACGGCCAGGGCCCTGAGGGCCCGAG 240  
Db 181 GATTACCTAGACATTTGCTGCCCTCCACTAGAACGGCCAGGGCCCTGAGGGCCCGAG 240  
QY 241 ACCTTTGCTTTGATGTTGAGTGGGCTGCTGCCAGGCTATGAGTCTGCCAGGAGGGCCCC 300  
Db 241 ACCTTTGCTTTGATGTTGAGTGGGCTGCTGCCAGGCTATGAGTCTGCCAGGAGGGCCCC 300  
QY 301 CGGGCCCTACAAGCGCTGGGTGCTCCCTGCCCTTTGGCCATGTTCAATTTCTCAGAGAAG 360  
Db 301 CGGGCCCTACAAGCGCTGGGTGCTCCCTGCCCTTTGGCCATGTTCAATTTCTCAGAGAAG 360  
QY 361 ATTACGCGCTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACTGGAGAGACTTACTAC 420  
Db 361 ATTACGCGCTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACTGGAGAGACTTACTAC 420  
QY 421 TACATCTCGGTGCCACTCCAGAGAGTTTCGGCCAGTGTGAGGCTCCAGGTGCTGTGTC 480  
Db 421 TACATCTCGGTGCCACTCCAGAGAGTTTCGGCCAGTGTGAGGCTCCAGGTGCTGTGTC 480  
QY 481 TGCTGCAAGGAGAGAGTCTGAGTCAAGCCATCTGTTGGGAGCCCTGGAGAGAGTGGC 540  
Db 481 TGCTGCAAGGAGAGAGTCTGAGTCAAGCCATCTGTTGGGAGCCCTGGAGAGAGTGGC 540  
QY 541 ACATCAGGTGGCGAGGGGGGACACTCCAGCCGCCCTCTGCTGCTTGTCTTACTGCTG 600  
Db 541 ACATCAGGTGGCGAGGGGGGACACTCCAGCCGCCCTCTGCTGCTTGTCTTACTGCTG 600  
QY 601 CTCTGATTTCTTCTGCTTCTGCGAATTTCTGTGAGCC 636  
Db 601 CTCTGATTTCTTCTGCTTCTGCGAATTTCTGTGAGCC 636

RESULT 5  
US-09-652-122-4283  
; Sequence 4283, Application US/09652122  
; GENERAL INFORMATION:  
; APPLICANT: Shyjan, Andrew W.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; FILE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.1194-001  
; CURRENT APPLICATION NUMBER: US/09/652,122  
; CURRENT FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/151,421



Query Match	99.7%;	Score 634.4;	DB 27;	length 1247;
Best Local Similarity	99.8%;	Pred. No. 6.3e-145;		
Matches 635;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps
QY	1	GCACAGACAAACCGGACTCGGGGGGATCGGCTGTGCTCCCTGTGCTGCGGAGACTGCTCTC 60		
Db	50	gccagaccaaaccgacctcgggcgatgcggtgctgccctgctcggaactgctc 109		
QY	61	TGGGCGCGTTCCTCGGCTCCCTCTGCGGGGGGCTCCAGCCTCCGCCACAGTAGTCTAC 120		
Db	110	tgggcgcttctcggtccccctcgcgggggtccagctccgcacgtagctctac 169		
QY	121	TGGAACCTCCAGTAACCCACAGTGTCTTCGAGAGAGACGCGTGTGAGCTGGGCCCTCAAC 180		
Db	170	tggaaacctcagtaacccccaggttgcttcgaggagacgcgtgagatcgggccctcaac 229		
QY	181	GATTACCTAGACATTTGCTCCGCCCCACTACGAAGGCCACAGGGCCCCCTGAGGGCCCCGAG 240		
Db	230	gattacctagacattgtgtccccactacgaagcccagggccccctgagggcccccgag 289		
QY	241	ACGTTTTCCTTTGACATGGTGGACTGGCCAGGCTATGAGTCTTCGCCAGCAGAGAGGCCCC 300		
Db	290	acgtttgctttgacatggtggactggcagggtatgagtccctggcaggcagagggcccc 349		
QY	301	CGGCGCTTACAAGCGCTGGGTGTGCTCCCTCCCTTTGGCCACTGTTCAATTCTCAGAGAAG 360		
Db	350	cgggcctacaagcgcgtgggtgctccctgccccttggccatgttcaattctcagagaag 409		
QY	361	ATTGAGGCGTTCACACCTTTCTCCCTCGGCTTTGAGTTCCTTACTCGAGAGACTTACTAC 420		
Db	410	attcagcgcttcacaccccttccccctgggttggatttcttaacctggagagactactac 469		
QY	421	TACATCTCGGTGGCCACTCCACAGAGATGTCGGCCAGTGCTGAGGCTTCCAGGTGTCTGTC 480		
Db	470	tacatctcgttgcccactccagagagtcttgccagtgcttgaggctccagtgctctg 529		
QY	481	TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCTCTGTTGGGAGCCCTGGAGAGAGTGCC 540		
Db	530	tgctgcaaggagaggaagtctgagtcagcccatctctgttgggagccctggagagagtggc 589		
QY	541	ACATCAGGCTGGCGAGGGGGGACATCTCCAGGCCCTCTGCTCTTGCTATTACTGCTGCTG 600		
Db	590	acatcagggttgggcgaggggggggggacactccagccccctctgtctcttacttactgctg 649		
QY	601	CTTCTGATTTCTCGCTCTCTCGCAATTTCTGTGAGCC 636		
Db	650	cttctgattctcgctctcttcgcaattctcttgagcc 685		

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RESULT      7
US-97-700-000-4952
; Sequence 4952, Application US/097000000
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2022-001
; CURRENT APPLICATION NUMBER: US/09/700,000
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,619
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 7171
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4952

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; LENGTH: 1247  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-700-000-4952

Query Match 99.7%; Score 634.4; DB 28; Length 1247;  
Best Local Similarity 99.8%; Pred. No. 6.3e-145;  
Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGACCAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCTGCTGGCGAGTGTCTC 60  
Db 50 gccagaccacaacggaacctcggggcgatgcygctgctgccccctgctggaagctgcctc 109  
QY 61 TGGGCCGCGTTCCTCGGCTCCCTCTCGCGGGGGGTCCAGCCTCGGCCACGCTAGTCTAC 120  
Db 110 tgggcccgcgttcctcgctccctctcgcgggggtccagcctcgccacgtagctctac 169  
QY 121 TGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGAGCCGCTGTGTGAGCTGGGCCCTCAAC 180  
Db 170 tgaactcceaagtaacccaggttgcttcgagagagccgctggtgagctgggacctcaac 229  
QY 181 GATTACTAGACATGTGTCGCCCCACTACGAAGGCCAGGGCCCTCGAGGGCCCGGAG 240  
Db 230 gatatactagacattgtctgccccccactacgaaggcccgggccccctgagggccccgag 289  
QY 241 ACCTTTGCTTTGATGATGTTGAGTGTGCTGCTGCCCTTTGGCCATGTTCAATCTCAGAGAAG 360  
Db 290 acgtttgctttgtacatggttgactggccaggtctatgagtcctgcccagggagggcccc 349  
QY 301 CGGGCTTACAGCGCTGGGTGCTGCTGCCCTTTGGCCATGTTCAATCTCAGAGAAG 360  
Db 350 cgggcttacaagcgctgggtgtgctccctgctcccttggccatgttcaattctcagaagaag 409  
QY 361 ATTCAGCGCTACACCTTTCTCCCTCGGCTTTGAGTCTTACCTCGAGAGACTTACTAC 420  
Db 410 attcagcgcttacaacctctccctcctgcttggcttggcttcttacctggagagacttactac 459  
QY 421 TACATCTCGGTGCCACTCCAGAGAGTCTTCGCCAGTGTCTTGAGGCTCCAGGCTGTCTGTC 480  
Db 470 tacatctcgttgcccactccagagagttcttggccagtgcttgaggtctccaggtgtctgtc 529  
QY 481 TGTGCAAGAGAGAGAGTCTGAGTCAGCCCATCTCTGTTGGGAGCCCTGGAGAGAGTGGC 540  
Db 530 tgtgcaagagaggaagtctgagtcagcccatctctgttggagccctggagagagtggc 589  
QY 541 ACATCAGGTTGGGAGGGGAGACTCCAGCCCTCTGCTGCTCTTGTCTATTACTGCTG 600  
Db 590 acatcaggggtggcgagggggggacactccagccccctctgtctctgtctattactgctg 649  
QY 601 CTTCTGATCTTCGCTTCTCGCAATTTCTGTAGCC 636  
Db 650 ctctgattcttcgtctcttcgtgaattctgtgagcc 685

RESULT 8  
US-09-760-443-311  
; Sequence 311, Application US/09760443  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJ212  
; CURRENT APPLICATION NUMBER: US/09/760,443  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 2164  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 311  
; LENGTH: 1273  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE

; LOCATION: (782)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (793)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (1069)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-760-443-311

Query Match 97.7%; Score 621.2; DB 30; Length 1273;  
Best Local Similarity 99.2%; Pred. No. 1.1e-141;  
Matches 631; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCCAGACCAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCTGCTGGCGAGTGTCTC 60  
Db 84 gccagaccacaacggaacctcggggcgatgcygctgctgccccctgctggaagctgcctc 143  
QY 61 TGGGCCGCGTTCCTCGGCTCCCTCTCGCGGGGGGTCCAGCCTCGGCCACGCTAGTCTAC 120  
Db 144 tgggcccgcgttcctcgctccctctcgcgggggtccagcctcgccacgtagctctac 203  
QY 121 TGAACCTCCAGTAACCCAGGTTGCTTCGAGGAGAGCCGCTGTGTGAGCTGGGCCCTCAAC 180  
Db 204 tgaactcceaagtaacccaggttgcttcgagagagccgctggtgagctgggacctcaac 263  
QY 181 GATTACTAGACATGTGTCGCCCCACTACGAAGGCCAGGGCCCTCGAGGGCCCGGAG 240  
Db 264 gattactagacattgtctgccccccactacgaaggcccgccccctgagggccccgag 323  
QY 241 ACCTTTGCTTTGATGATGTTGAGTGTGCTGCTGCCCTTTGGCCATGTTCAATCTCAGAGAAG 360  
Db 324 acgtttgctttgtacatggttgactggccaggtctatgagtcctgcccagggagggcccc 383  
QY 301 CGGGCTTACAGCGCTGGGTGCTGCTGCCCTTTGGCCATGTTCAATCTCAGAGAAG 360  
Db 384 cgggcttacaagcgctgggtgtgctccctgctcccttggccatgttcaattctcagaagaag 443  
QY 361 ATTCAGCGCTTACACCTTTCTCCCTCGGCTTTGAGTCTTACCTCGAGAGACTTACTAC 420  
Db 444 attcagcgcttacaacctctccctcctgcttggcttggcttcttacctggagagacttactac 503  
QY 421 TACATCTCGGTGCCACTCCAGAGAGTCTTCGCCAGTGTCTTGAGGCTCCAGGCTGTCTGTC 480  
Db 504 tacatctcgttgcccactccagagagttcttggccagtgcttgaggtctccaggtgtctgtc 563  
QY 481 TGTGCAAGAGAGAGAGTCTGAGTCAGCCCATCTCTGTTGGGAGCCCTGGAGAGAGTGGC 540  
Db 564 tgtgcaa-gagaggaagtctgagtcagcccatctctgttggagccctggagagagtggc 622  
QY 541 ACATCAGGTTGGGAGGGGAGACTCCAGCCCTCTGCTGCTCTTGTCTATTACTGCTG 600  
Db 623 acatcaggggtggcgagggggggacactccagccccctctgtctcttcttcttactgctg 682  
QY 601 CTTCTGATCTTCGCTTCTCGCAATTTCTGTAGCC 636  
Db 683 ctctgattcttcgtctcttcgtgaattctgtgagcc 718

RESULT 9  
US-09-306-609-7629  
; Sequence 7629, Application US/09306609  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-718CON2  
; CURRENT APPLICATION NUMBER: US/09/306,609  
; CURRENT FILING DATE: 1999-05-07  
; EARLIER APPLICATION NUMBER: US 09/168,296  
; EARLIER FILING DATE: 1998-10-07  
; EARLIER APPLICATION NUMBER: US 08/949,553

```

; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 13025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7629
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(531)
; OTHER INFORMATION: n = A,T,C or G
US-09-306-609-7629

```

```

Query Match      73.8%; Score 469.4; DB 17; Length 531;
Best Local Similarity 99.2%; Pred. No. 1.4e-104;
Matches 481; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 12 CCGGACCTCGGGGGGATGCGGCTGCTGCCCTGCTGCGGACTGTCCTCTGGGCGCGTT 71
Db 1 ceggaacctcgggggcgatgcggtgctgccccctgctgcgactgctctggcgcgctt 60

Qy 72 CCTCGGCTCCCTCTGCGGGGGGCTCCAGCTCGGCCACAGTAGTCTACTGGAATCCAG 131
Db 61 cctcggtccccctctgctgcggggtccagctccgacgtagctactggaactccag 120

Qy 132 TAACCCAGAGTTGCTTTCGAGGAGAGCGCGTGTGAGCTGGGCGCTCAAGATTACCTAGA 191
Db 121 taacccagagttgcttgcgagagagcggtggtgagctggggtcccaacgattacctaga 180

Qy 192 CATTTCTGCCCCACTACGAAGGCCAGGCCCCCTGAGGCCCCCGGAGAGCTTTGCTTT 251
Db 181 cattgtcgtccccactacgaagggccccctgagggcccccgagagcttgcgtt 240

Qy 252 GTACATGTGGAGTGGCGAGGCTATGAGTCTGCGGAGGCCCCCGGCGCTACAA 311
Db 241 gtacatgtggagtgccaggtatgagtcctgagggcccccgagagggcccccgctacaa 300

Qy 312 GCGCTGGGTGCTCCCTGCGGCTTTGGGCATGTTCAATTCTCAGAGAGATTTCAGCGGTT 371
Db 301 gcgctgggtgctccctgcccccttggccatgttcaattctcagagagatttcagcgctt 360

Qy 372 CACACCTTTCTCCCTCGGCTTTGAGTTCTTACTTGAGAGACTTACTACTACATCTCGGT 431
Db 361 cacaccttctccctcggttggcttacttacttgagagacttactactacatctcgtt 420

Qy 432 GCCCACTCCAGAGATTCTGGCCAGTGTGAGGCTCCAGGTGCTGCTGCTGCAAGGA 491
Db 421 gcccactccagagattcttgg-cagtgtgaggtccangtctgtctgctgcaagga 479

Qy 492 GAGGA 496
Db 480 ganga 484

```

```

RESULT 10
US-09-522-251-7629
; Sequence 7629, Application US/09522251
; GENERAL INFORMATION:
; APPLICANT: Dmanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark C.
; APPLICANT: Jones, Lee W.
; APPLICANT: Garcia, Veronica E.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 718CIP
; CURRENT APPLICATION NUMBER: US/09/522,251
; PRIOR FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: 09/306,609
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: 09/168,296

```

```

; EARLIER FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: 60/150,686
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 13025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7629
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(531)
; OTHER INFORMATION: n = A,T,C or G
US-09-522-251-7629

```

```

Query Match      73.8%; Score 469.4; DB 19; Length 531;
Best Local Similarity 99.2%; Pred. No. 1.4e-104;
Matches 481; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 12 CCGGACCTCGGGGGGATGCGGCTGCTGCCCTGCTGCGGACTGTCCTCTGGGCGCGTT 71
Db 1 ceggaacctcgggggcgatgcggtgctgccccctgctgcgactgctcttggcgcgctt 60

Qy 72 CCTCGGCTCCCTCTGCGGGGGGCTCCAGCTCGGCCACAGTAGTCTACTGGAATCCAG 131
Db 61 cctcggtccccctctgctgcggggtccagctccgacgtagctactggaactccag 120

Qy 132 TAACCCAGAGTTGCTTTCGAGGAGAGCGCGTGTGAGCTGGGCGCTCAAGATTACCTAGA 191
Db 121 taacccagagttgcttgcgagagagcggtggtgagctggggtcccaacgattacctaga 180

Qy 192 CATTTCTGCCCCACTACGAAGGCCAGGCCCCCTGAGGCCCCCGGAGAGCTTTGCTTT 251
Db 181 cattgtcgtccccactacgaagggccccctgagggcccccgagagcttgcgtt 240

Qy 252 GTACATGTGGAGTGGCGAGGCTATGAGTCTGCGGAGGCCCCCGGCGCTACAA 311
Db 241 gtacatgtggagtgccaggtatgagtcctgagggcccccgagagggcccccgctacaa 300

Qy 312 GCGCTGGGTGCTCCCTGCGGCTTTGGGCATGTTCAATTCTCAGAGAGATTTCAGCGGTT 371
Db 301 gcgctgggtgctccctgcccccttggccatgttcaattctcagagagatttcagcgctt 360

Qy 372 CACACCTTTCTCCCTCGGCTTTGAGTTCTTACTTGAGAGACTTACTACTACATCTCGGT 431
Db 361 cacaccttctccctcggttggcttacttacttgagagacttactactacatctcgtt 420

Qy 432 GCCCACTCCAGAGATTCTGGCCAGTGTGAGGCTCCAGGTGCTGCTGCTGCAAGGA 491
Db 421 gcccactccagagattcttgg-cagtgtgaggtccangtctgtctgctgcaagga 479

Qy 492 GAGGA 496
Db 480 ganga 484

```

```

RESULT 11
US-10-025-600-7629
; Sequence 7629, Application US/10025600
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-718CON2
; CURRENT APPLICATION NUMBER: US/10/025,600
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/306,609
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/168,296
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/949,553
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-09

```

```
; NUMBER OF SEQ ID NOS: 13025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7629
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(531)
; OTHER INFORMATION: n = A,T,C or G
US-10-025-600-7629
```

```
Query Match          73.8%; Score 469.4; DB 37; Length 531;
Best Local Similarity 99.2%; Pred. No. 1.4e-104;
Matches 481; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 12 CCGGACCTCGGGGGCGATGCGGCTGCTGCCCCCTGCTGCGGACTGCTCTCTGGGCCCGGTT 71
Db 1 cgggaactcggggcgatcggtctgctgccccctgctggaactgctctctgggcccgtt 60

QY 72 CTTCTGGCTCCCTCTGCGGGGGCTCCAGCCCTCCGCGCTAGTCTACTTGGAACTCCAG 131
Db 61 cctcggctccccctctcgcggggctccagcctcccgactagcttaactggaaactccag 120

QY 132 TAACCCACAGTTCCTTCGAGGAGACCCGCTGGTGGAGCTGGGCTCAACGATTACCTAGA 191
Db 121 taacccacagttgcttcgaggagacgcgctggtggagctgggacctcaacgattaccta 180

QY 192 CATTTGCTGCCCCACTAGAACGCCAGGCCCTGAGGCCCTGAGGCCCTGAGGCTTTCCTTT 251
Db 181 catgtctgccccactacgaagggccagggccccctgagggccccgagacgtttgcttt 240

QY 252 GTACATGGTGGACTGCCAGGCTATGAGTCTGCCAGGAGAGGCCGCCGGGSCCTACAA 311
Db 241 gtacatggtggagctggccagggctatgagtcctcgccaggcagaggccccccggccacaa 300

QY 312 GCCTGGGTGTCTCCCTGCCCTTGGCCATGTTCAATTCTCAGAGAAGATTTCAGCGCTT 371
Db 301 gcgctgggtgtctccctgccccttggccatgttcaattctcagagaagatttcagcgctt 360

QY 372 CACACCTTCTCCCTCGGCTTTGAGTCTTACCTGAGAGACTTACTACTACTCTCGGT 431
Db 361 cacacctctccctcggtttgagttcttacctgagagacttactactactctcgtt 420

QY 432 GCCACTCCAGAGTTCGCGCAGTGTGAGCTTCCAGGCTCCTGCTGCTGCAAGGA 491
Db 421 gccactccagagagttctgg-cagtgcttgagggtccccangtctgtctgtcgtcgaagga 479

QY 492 GAGGA 496
Db 480 ganga 484
```

```
RESULT 12
US-09-205-070-27545
; Sequence 27545, Application US/09205070
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748
; CURRENT APPLICATION NUMBER: US/09/205,070
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27545
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(532)
```

```
; OTHER INFORMATION: n = A,T,C or G
US-09-205-070-27545

Query Match          73.8%; Score 469.4; DB 16; Length 532;
Best Local Similarity 99.2%; Pred. No. 1.4e-104;
Matches 481; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 12 CCGGACCTCGGGGGCGATGCGGCTGCTGCCCCCTGCTGCGGACTGCTCTCTGGGCCCGGTT 71
Db 2 ccggaaactcggggcgatcggtctgctgccccctgctggaactgctctctcggaactcgtt 61

QY 72 CTTCTGGCTCCCTCTGCGGGGGCTCCAGCCCTCCGCGCTAGTCTACTTGGAACTCCAG 131
Db 62 cctcggctccccctctcgcggggctccagcctccggcagctagcttaactggaaactccag 121

QY 132 TAACCCACAGTTCCTTCGAGGAGACCCGCTGGTGGAGCTGGGCTCAACGATTACCTAGA 191
Db 122 taacccacagttgcttcgaggagacgcgctggtggagctgggacctcaacgattaccta 181

QY 192 CATTTGCTGCCCCACTAGAACGCCAGGCCCTGAGGCCCTGAGGCCCTGAGGCTTTCCTTT 251
Db 182 catgtctgccccactacgaagggccccctgagggccccccgagacgtttgcttt 241

QY 252 GTACATGGTGGACTGCCAGGCTATGAGTCTGCCAGGAGAGGCCGCCGGGSCCTACAA 311
Db 242 gtacatggtggagctggccaggtatgagtcctgcccaggcagaggccccccgggacctcaa 301

QY 312 GCCTGGGTGTCTCCCTGCCCTTGGCCATGTTCAATTCTCAGAGAAGATTTCAGCGCTT 371
Db 302 gcgctgggtgtctccctgccccttggccatgttcaattctcagagaagatttcagcgctt 361

QY 372 CACACCTTCTCCCTCGGCTTTGAGTCTTACCTGAGAGACTTACTACTACTCTCGGT 431
Db 362 cacacctctccctcggtttgagttcttacctgagagacttactactactctcgtt 421

QY 432 GCCACTCCAGAGTTCGCGCAGTGTGAGCTTCCAGGCTCCTGCTGCTGCAAGGA 491
Db 422 gccactccagagagttctgg-cagtgcttgagggtccccangtctgtctgtcgtcgaagga 480

QY 492 GAGGA 496
Db 481 ganga 485
```

```
RESULT 13
US-09-340-623-27545
; Sequence 27545, Application US/09340623
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/340,623
; CURRENT FILING DATE: 1999-06-28
; EARLIER APPLICATION NUMBER: US 09/205,070
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27545
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(532)
; OTHER INFORMATION: n = A,T,C or G
US-09-340-623-27545

Query Match          73.8%; Score 469.4; DB 17; Length 532;
Best Local Similarity 99.2%; Pred. No. 1.4e-104;
Matches 481; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
```

QY 12 CCGGACCTCGGGGGGATCGGCTGCTGCCCTGCTGGGACTGCTCTGGGCGCGCTT 71  
|||||  
Db 2 ccggacctcggggcgatcgctgctgccccctgctcgactgctccttggcgcgctt 61  
|||||  
QY 72 CTTGCTGCTCCCTCTGCGGGGGGCTCCAGCTCGGCTCGGCTAGTCTACTGAACTCCAG 131  
|||||  
Db 62 cctcgctccccctctgctgctgggggctccagctccgcaagtagtctactggaactccag 121  
|||||  
QY 132 TAACCCAGCTGCTTCGAGGAGACGCGCTGCTGGAGCTGGCCCTCAAGATTACTAGA 191  
|||||  
Db 122 taacccaggttgcttcgagagagacgctgctggagctgggctccaaacgattactacga 181  
|||||  
QY 192 CATTTGCTCCCTCCCTACAGAGGCCCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTT 251  
|||||  
Db 182 cattgctgccccactacgaagggccagggccccctgagggccccgagacgtttgcttt 241  
|||||  
QY 252 GTACATGCTGGAGCTGGCCAGGCTATGAGTCTCCAGGAGAGAGGCCCCCGGCTTACAA 311  
|||||  
Db 242 gtacatggtggactggcaggctatgagtcctgcccagggagggccccggcctacaa 301  
|||||  
QY 312 GCGCTGGGTGCTCCCTCGGCTTTGAGTCTTCAATTTCTCAGAGAGATTTCAGGCTT 371  
|||||  
Db 302 ggcctgggtgctccctgctcccttggccatgttcaattctcagagagattcagcgctt 361  
|||||  
QY 372 CACACTTTCTCCCTCGGCTTTGAGTCTTCAATTTCTCAGAGAGATTTCAGTCTCGT 431  
|||||  
Db 362 cacaccttctccctcgcttggcttggcttcttacttgagagacttactactactcctcgt 421  
|||||  
QY 432 GCCACTCCAGAGAGTTCTGGCCAGTCTGAGGCTCCAGGCTGCTGCTGCTGCAAGGA 491  
|||||  
Db 422 gccactccagagagttctgg-cagtgttgaggctccangtctgtctgtgcaagga 480  
|||||  
QY 492 GAGGA 496  
|| ||  
Db 481 ganga 485

## RESULT 14

US-09-898-888-27545  
; Sequence 27545, Application US/09898888  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA  
; FILE OF INVENTION: LIBRARIES  
; FILE REFERENCE: 20411-748CON1  
; CURRENT APPLICATION NUMBER: US/09/898,888  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/340,623  
; PRIOR FILING DATE: 1999-06-28  
; NUMBER OF SEQ ID NOS: 45207  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27545  
; LENGTH: 532  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(532)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-898-888-27545

Query Match 73.8%; Score 459.4; DB 33; Length 532;

Best Local Similarity 99.2%; Pred. No. 1.4e-104;  
Matches 481; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 12 CCGGACCTCGGGGGGATCGGCTGCTGCCCTGCTGGGACTGCTCTGGGCGCGCTT 71  
|||||  
Db 2 ccggacctcggggcgatcgctgctgccccctgctcgactgctccttggcgcgctt 61  
|||||  
QY 72 CTTGCTGCTCCCTCTGCGGGGGGCTCCAGCTCGGCTCGGCTAGTCTACTGAACTCCAG 131  
|||||

Db 62 cctcgctccccctctgctgctgggggctccagctccgcaagtagtctactggaactccag 121  
|||||  
QY 132 TAACCCAGCTGCTTCGAGGAGACGCGCTGCTGGAGCTGGCCCTCAAGATTACTAGA 191  
|||||  
Db 122 taacccaggttgcttcgagagagacgctgctggagctgggctccaaacgattactacga 181  
|||||  
QY 192 CATTTGCTCCCTCCCTACAGAGGCCCGGCTCGGCTCGGCTCGGCTCGGCTT 251  
|||||  
Db 182 cattgctgccccactacgaagggccagggccccctgagggccccgagacgtttgcttt 241  
|||||  
QY 252 GTACATGCTGGAGCTGGCCAGGCTATGAGTCTCCAGGAGAGAGGCCCCCGGCTTACAA 311  
|||||  
Db 242 gtacatggtggactggcaggctatgagtcctgcccagggagggccccggcctacaa 301  
|||||  
QY 312 GCGCTGGGTGCTCCCTCGGCTTTGAGTCTTCAATTTCTCAGAGAGATTTCAGGCTT 371  
|||||  
Db 302 ggcctgggtgctccctgctcccttggccatgttcaattctcagagagattcagcgctt 361  
|||||  
QY 372 CACACTTTCTCCCTCGGCTTTGAGTCTTCAATTTCTCAGAGAGATTTCAGTCTCGT 431  
|||||  
Db 362 cacaccttctccctcgcttggcttggcttcttacttgagagacttactactactcctcgt 421  
|||||  
QY 432 GCCACTCCAGAGAGTTCTGGCCAGTCTGAGGCTCCAGGCTGCTGCTGCTGCAAGGA 491  
|||||  
Db 422 gccactccagagagttctgg-cagtgttgaggctccangtctgtctgtgcaagga 480  
|||||  
QY 492 GAGGA 496  
|| ||  
Db 481 ganga 485

## RESULT 15

US-09-898-888A-27545  
; Sequence 27545, Application US/09898888A  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA  
; FILE OF INVENTION: LIBRARIES  
; FILE REFERENCE: 20411-748CON1  
; CURRENT APPLICATION NUMBER: US/09/898,888A  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/340,623  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/205,070  
; PRIOR FILING DATE: 1998-12-03  
; NUMBER OF SEQ ID NOS: 45207  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27545  
; LENGTH: 532  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(532)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-898-888A-27545

Query Match 73.8%; Score 459.4; DB 33; Length 532;

Best Local Similarity 99.2%; Pred. No. 1.4e-104;  
Matches 481; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 12 CCGGACCTCGGGGGGATCGGCTGCTGCCCTGCTGGGACTGCTCTGGGCGCGCTT 71  
|||||  
Db 2 ccggacctcggggcgatcgctgctgccccctgctcgactgctccttggcgcgctt 61  
|||||  
QY 72 CTTGCTGCTCCCTCTGCGGGGGGCTCCAGCTCGGCTCGGCTAGTCTACTGAACTCCAG 131  
|||||  
Db 62 cctcgctccccctctgctgctgggggctccagctccgcaagtagtctactggaactccag 121  
|||||  
QY 132 TAACCCAGCTGCTTCGAGGAGACGCGCTGCTGGAGCTGGCCCTCAAGATTACTAGA 191  
|||||  
Db 122 taacccaggttgcttcgagagagacgctgctggagctgggctccaaacgattactacga 181  
|||||



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OM nucleic - nucleic search, using sw model

Run on: September 28, 2002, 01:35:23 ; Search time 401.97 Seconds  
(without alignments)  
5139.396 Million cell updates/sec

Title: US-09-904-954-3  
Perfect score: 636  
Sequence: 1 GCCAGACCAACCGGACCTC.....TTCTGCAATTCGTGAGCC 636

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2167403 seqs, 1624121725 residues  
Total number of hits satisfying chosen parameters: 4334806

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	636	100.0	636	5	US-09-053-375B-187
2	636	100.0	636	5	US-09-440-302B-839
3	621.2	97.7	1273	6	US-10-206-021-271
4	621.2	97.7	1273	6	US-10-212-054-311
5	357	56.1	472	5	US-09-918-995-20569
6	317	49.8	481	7	US-10-142-593-207
7	288.6	45.4	5831	6	US-10-206-021-924
8	288.6	45.4	5831	6	US-10-212-054-1809
9	267	42.0	267	5	US-09-442-366A-548
10	267	42.0	267	5	US-09-440-302B-242
11	143.4	22.5	771	7	US-10-027-632-32020
12	103.4	16.3	987	1	PCT-US02-25766-6624
13	103.4	16.3	987	5	US-09-053-375B-186
14	103.4	16.3	987	5	US-09-440-302B-838
15	101.8	16.0	1480	1	PCT-US02-13644-14
16	101.8	16.0	1480	5	US-09-053-375B-1504
17	101.8	16.0	1480	5	US-09-442-384B-743
18	101.8	16.0	1480	5	US-09-440-302B-837
19	101.8	16.0	1480	7	US-10-007-926A-227
20	101.8	16.0	1480	7	US-10-136-819-14
21	101.8	16.0	1480	7	US-10-171-311-49
22	101.8	16.0	1480	7	US-10-171-581-190
23	101.8	16.0	1496	1	PCT-US02-24563-287
24	101.8	16.0	1496	6	US-10-194-359-287
25	101.8	16.0	1496	6	US-10-192-007-287

26	101.8	16.0	1496	6	US-10-210-951-39	Sequence 39, Appl
27	101.8	16.0	1496	6	US-10-211-858-39	Sequence 39, Appl
28	101.8	16.0	1496	6	US-10-211-884-39	Sequence 39, Appl
29	101.8	16.0	1496	6	US-10-230-417-287	Sequence 287, App
30	101.8	16.0	1496	7	US-10-121-049-287	Sequence 287, App
31	101.8	16.0	1496	7	US-10-121-050-287	Sequence 287, App
32	101.8	16.0	1496	7	US-10-121-053-287	Sequence 287, App
33	101.8	16.0	1496	7	US-10-121-043-287	Sequence 287, App
34	101.8	16.0	1496	7	US-10-121-044-287	Sequence 287, App
35	101.8	16.0	1496	7	US-10-121-047-287	Sequence 287, App
36	101.8	16.0	1496	7	US-10-121-054-287	Sequence 287, App
37	101.8	16.0	1496	7	US-10-121-056-287	Sequence 287, App
38	101.8	16.0	1496	7	US-10-121-057-287	Sequence 287, App
39	101.8	16.0	1496	7	US-10-121-058-287	Sequence 287, App
40	101.8	16.0	1496	7	US-10-121-060-287	Sequence 287, App
41	101.8	16.0	1496	7	US-10-121-063-287	Sequence 287, App
42	101.8	16.0	1496	7	US-10-123-108-287	Sequence 287, App
43	101.8	16.0	1496	7	US-10-123-134-287	Sequence 287, App
44	101.8	16.0	1496	7	US-10-123-156-287	Sequence 287, App
45	101.8	16.0	1496	7	US-10-123-157-287	Sequence 287, App

ALIGNMENTS

RESULT 1  
US-09-053-375B-187  
; Sequence 187, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; FILE REFERENCE: CLON-006  
; CURRENT APPLICATION NUMBER: US/09/053,375B  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 187  
; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-053-375B-187

Query Match	100.0%	Score 636;	DB 5;	Length 636;
Best Local Similarity	100.0%	Pred. No. 7.8e-142;		
Matches 636;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GCAGACCAACCGGACCTCGGGGGGATGCGGCTGCTGCCCTGCTGCGGACTGCTCTTC	60	
Db	1	gccagaccacacccgacacctcgggggcgatgcgctgctgccccctgctgagactgtcttc	60	
Qy	61	TGGGGCGGTTCCTCGGCTCCCTCTGCGGGGGCTCGAGCTCGGCGACCTAGTCTAC	120	
Db	61	tgggcgcgttctctcgctccctctgcgggggctccagctcgcgcacgtactctac	120	
Qy	121	TGGAACCTCAGTAACCCAGAGTTGTTGAGGAGACGGCTGGTGGAGCTGGGCTCAAC	180	
Db	121	tgggaactccagtaaccccaaggctgtctcgaggagacgcgctggtagctggggctcaac	180	
Qy	181	GATTACCTAGACATTTCTGCCCCCCTACAGAGCCCGGAGGCCCCCTGAGGCCCCGAG	240	
Db	181	gattacctagacatgtctgccccactacgaagcccgagggccccctgagggccccgag	240	
Qy	241	ACGTTTGTGTTTACATGTTGAGTGGCGAGCTATGAGTCTGCGAGGACGAGGCCCC	300	
Db	241	acgtttgtgtttatagttggaactggcaggctatgagctcctgcaggagagggcccc	300	
Qy	301	CGGGCCTACAACGCGTGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCACAGAG	360	
Db	301	cgggcctacaagcgtgggtgtgctccctgcccccttggcca tgttcaattccagaga	360	
Qy	361	ATTACGCGTTTACACACCTTTCTCCCTCGGCTTTGAGTTTACCTTGAGAGACTTACTAC	420	

```
Db 361 attcagcgttcacacattcttctccctcggtttgagttcttactctgagagacttactac 420
QY 421 TACATCTCGGTGCCACTCCAGAGAGTTCTGGCCAGTGTCTGAGGCTCCAGGTCTGCTGTC 480
Db 421 tacatctcgggtgccactccagagagttcttggccagtgttggaggtccagggtgtctgtc 480
QY 481 TGCTCAAGAGAGAGAGTCTGAGTCAGCCATCCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
Db 481 tgctgcaagagagagagagagagagagagagagagagagagagagagagagagagag 540
QY 541 ACATCAGGTGGCGAGGGGGGACATCCAGAGCCCTCTGCTCTGCTTATTTACTGCTG 600
Db 541 acatcagagagagagagagagagagagagagagagagagagagagagagagagag 600
QY 601 CTCTGATCTCTGCTCTGCGAATTTCTGTGAGCC 636
Db 601 ctctgattctctgctctctcggaattctgtgagcc 636

RESULT 2
US-09-440-302B-839
; Sequence 839, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 839
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-440-302B-839

Query Match 100.0%; Score 636; DB 5; Length 636;
Best Local Similarity 100.0%; Pred. No. 7.8e-142; Indels 0; Gaps 0;
Matches 636; Conservative 0; Mismatches 0;

QY 1 GCCAGACCAACCGGACCTCGGGGGCGATCGCGCTGCTGCCCCCTGCTGCGAGACTGCTC 60
Db 1 gccagaccacacggacctcgggcgagatcggtctgcccctgctgagactgtcctc 60
QY 61 TGGGCGCGTTCCTGCGCTCCCTCTGCGGGGGGTCCAGCCTCCGCCACGTAGTCTAC 120
Db 61 tgggcccgttctcgtgctccctctgcccgggggtccagcctccgccacgtagtctac 120
QY 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGAGAGCGCCGTGTTGGAGCTGGGCCCTCAAC 180
Db 121 tggaaactccagtaacccaggttgcttcgagagagacgcgtgtgtgagctgggacctcaac 180
QY 181 GATTACCTAGACATTGCTGCCCCACTACGAAGGCCAGGGCCCCCTGAGGGCCCCGAG 240
Db 181 gattacctagacattgctgccccactacgaaggccagggccccctgagggcccccgag 240
QY 241 ACCTTTGCTTTGATGTTGAGTGGCTAGGCTATGAGTCTGCCAGGCGAGGGCCCC 300
Db 241 acgtttgctttgacatggtgagctggccaggtatgagtcctgccaggcagaggcccc 300
QY 301 CGGGCTACAGAGCGGTGGTGGCTGCTGCCCTTTGGCCATGTTCAATTTCTCAGAGAAG 360
Db 301 cgggctacagagcggtgggtggctgctgccctttggccatgttcaattctcagagaag 360
QY 361 ATTACGGCTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACTCTGAGAGACTTACTAC 420
Db 361 attacggcttacacctttctccctcggctttgagttcttactctggagagacttactac 420
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QY 421 TACATCTCGGTGCCACTCCAGAGAGTTCTGGCCAGTGTCTGAGGCTCCAGGTCTGCTGTC 480
Db 421 tacatctcgggtgccactccagagagttcttggccagtgttggaggtccagggtgtctgtc 480
QY 481 TGCTCAAGAGAGAGAGTCTGAGTCAGCCATCCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
Db 481 tgctgcaagagagagagagagagagagagagagagagagagagagagagagagagag 540
QY 541 ACATCAGGTGGCGAGGGGGGACATCCAGAGCCCTCTGCTCTGCTTATTTACTGCTG 600
Db 541 acatcagagagagagagagagagagagagagagagagagagagagagagagagag 600
QY 601 CTCTGATCTCTGCTCTGCGAATTTCTGTGAGCC 636
Db 601 ctctgattctctgctctctcggaattctgtgagcc 636

RESULT 3
US-10-206-021-271
; Sequence 271, Application US/10206021
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT251CIN
; CURRENT APPLICATION NUMBER: US/10/206,021
; CURRENT FILING DATE: 2002-07-29
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 937
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (782)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (793)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1069)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-206-021-271

Query Match 97.7%; Score 621.2; DB 6; Length 1273;
Best Local Similarity 99.2%; Pred. No. 2.8e-138;
Matches 631; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCCAGACCAACCGGACCTCGGGGGCGATCGCGCTGCTGCCCCCTGCTGCGAGACTGCTC 60
Db 84 gccagaccacacacggacctcgggcgagatcggtctgcccctgctgagactgtcctc 143
QY 61 TGGGCGCGTTCCTGCGCTCCCTCTGCGGGGGGTCCAGCCTCCGCCACGTAGTCTAC 120
Db 144 tgggcccgttctcgtgctccctctgcccgggggtccagcctccgccacgtagtctac 203
QY 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGAGAGCGCGTGTGAGCTGGGCCCTCAAC 180
Db 204 tggaaactccagtaacccaggttgcttcgagagagacgcgtgtgtgagctgggacctcaac 263
QY 181 GATTACCTAGACATTGCTGCCCCACTACGAAGGCCAGGGCCCCCTGAGGGCCCCGAG 240
Db 264 gattacctagacattgctgccccactacgaaggccccctgagggcccccgag 323
QY 241 ACCTTTGCTTTGATGTTGAGTGGCTAGGCTATGAGTCTGCCAGGCGAGGGCCCC 300
Db 324 acgtttgctttgacatggtgagctggccaggtatgagtcctgccaggcagaggcccc 363
QY 301 CGGGCTACAGAGCGGTGGGTGGTGGCTGCTGCCCTTTGGCCATGTTCAATTTCTCAGAGAAG 360
```



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Db 384 cgggctacaagcgtgggtgtgtccctgccccttggccatgttcaattctcagagaag 443
QY 361 ATTACAGCGTTACACACTTCTCCCTCGGCTTGTAGCTTCTTACTCGAGAGACTTACTAC 420
Db 444 attcagcgttccamacccttctccctcggtctttraggcttcttacttgagagacttactac 503
QY 421 TACATCTCGGTGCCACTCCAGAGAGTCTTGCCCACTGTGGCCAGTGTGAGGCTCCAGGTGTCTGTC 480
Db 504 tacatctcgtgtgccactccagagagtcttgccagtgctgaggtccagggtgtctgtc 563
QY 481 TGTCTCAAGGAGAGAACTGTAGTTCAGCCCATCTCTGTTGGGAGCCCTCGAGAGAGTGGC 540
Db 564 tgtgtcaa-gagaggaagtctgagtcagcccatctctgttggagccctggagagagtgc 622
QY 541 ACATCAGGTGGGAGGGGGAGACTCCAGCCCTCTGTCTCTTGTCTTACTTACTGCTG 600
Db 623 acatcagggtgagcaggggggagacatccagccctctgtctcttcttattactgctg 682
QY 601 CTCTCATCTTCTGCTTCTTGTGCAATCTGTGAGCC 636
Db 683 ctctgatctctgtctcttcttggaattctgtgagcc 718

RESULT 4
US-10-212-054-311
; Sequence 311, Application US/10212054
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ12CIN
; CURRENT APPLICATION NUMBER: US/10/212,054
; NUMBER OF SEQ ID NOS: 2164
; Prior application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 311
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (782)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (793)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1069)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-212-054-311

Query Match 97.7%; Score 621.2; DB 6; Length 1273;
Best Local Similarity 99.2%; Pred. No. 2.8e-138;
Matches 631; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCCAGACCAACCGGACCTCGGGGGGATGCGGCTGTCGCCCTGCTGGGACTGTCCTC 60
Db 84 gccagaccacaacccgacctcggggcgatgctgctgctgctgctgctgctgctc 143
QY 61 TGGCCCGCGTTCCTCGGCTCCCTCTGCGGGGGGTCCAGCCCTCGCCACGAGTCTAC 120
Db 144 tgggcccgcgtctctcggtccctctctgcgcgggggtccagcctccgcacgtagtctac 203
QY 121 TGAACCTCCAGTAACCCCGAGTGTCTTCGAGGAGAGCCGCTGTGTGAGGTGGCCCTCAAC 180
Db 204 tggaaactccagtaaccccgagttgcttcagagagacgcgtggtgagctgggacctcaac 263
QY 181 GATTACTTAGACATGTGTGTCGCCCCCACTACGAAGGCCAGGGCCCTCGAGGCCCGCGAG 240
|||||
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Db 264 gattacctagacattgtctgtccccactacgaagggccccctgagggccccgag 323
QY 241 ACCTTTGCTTTGTACATGTGGACTGGCAGGCTATGAGTCTGTCAGGACGAGGGCCCC 300
Db 324 acgtttgtttacatggtgagctgcccagctatgagctctccagcagagggcccc 383
QY 301 CGGGCCTACAAGGCTTGGGTGTGCTCCCTGCGCTTGGGCATGTTCAATTCTCAGAGAG 360
Db 384 cgggctacaagcgtgggtgtgtccctgccccttggccatgttcaattctcagagaag 443
QY 361 ATTCAGCGCTTCACACCTTCTCCCTCGGCTTGTAGCTTCTTACTCGAGAGACTTACTAC 420
Db 444 attcagcgttccamacccttctccctcggtctttraggcttcttacttgagagacttactac 503
QY 421 TACATCTCGGTGCCACTCCAGAGAGTCTTGCCCACTGTGAGGCTCCAGGCTGTCTGTC 480
Db 504 tacatctcgtgtgccactccagagagtcttgccagtgctgaggtccagggtgtctgtc 563
QY 481 TGTCTCAAGGAGAGAACTGTAGTTCAGCCCATCTCTGTTGGGAGCCCTCGAGAGAGTGGC 540
Db 564 tgtgtcaa-gagaggaagtctgagtcagcccatctctgttggagccctggagagagtgc 622
QY 541 ACATCAGGTGGGAGGGGGAGACTCCAGCCCTCTGTCTCTTGTCTTACTTACTGCTG 600
Db 623 acatcagggtgagcaggggggagacatccagccctctgtctcttcttattactgctg 682
QY 601 CTCTCATCTTCTGCTTCTTGTGCAATCTGTGAGCC 636
Db 683 ctctgatctctgtctcttcttggaattctgtgagcc 718

RESULT 5
US-09-918-995-20569
; Sequence 20569, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20569
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(472)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-20569

Query Match 56.1%; Score 357; DB 5; Length 472;
Best Local Similarity 98.4%; Pred. No. 1.8e-75;
Matches 360; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 271 GGCTATGATGTCCTGCGCAGGAGAGGCCCGGCTTACAGCGCTGGGTGTGCTCCCTG 330
Db 22 gtagacgagtcctcgccagcagaggcccccgggcccataaagcgtgggtgtgctccctg 81
QY 331 CCCTTTGGCCATGTTCAATCTTCAGAGAGATTTCAGCGCTTCACACTTCTCCCTCGGC 390
Db 82 ccccttggccatgttcaattctcagagaagtcagcgccttcacaccttctccctcggc 141
QY 391 TTTGAGTCTTACTCGAGAGACTTACTACTACTACTCGGTGCCCTCCACTCCAGAGAGTCT 450
Db 142 ttgtgattcttactctggagagacttactactatctcgtggtccactccagagagttct 201
QY 451 GGCCAGTGTCTGAGGCTCCAGGTGTCTGTCTGTCGAAGGAGAGAGAGTCTGAGTCAGCC 510
|||||
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QY 198 CTGCCCCCTACGAGCCCGCAGGCCCCCTGAGGCCCCGAGAGCTTTGCTTTGTACAT 257
|||||
Db 3062 ctgcccccaactacgaagcccgagccccctgagggccccgagagctttgtttgtacat 3121
QY 258 GGTGACTGGCCAGGCTATGAGTCTGCGCAGCAGGAGGCCCCCGGCGCTACAGCGGTG 317
|||||
Db 3122 ggtgactggccaggtatgagctctgcagcgagagggccccggcgctacaagcgtg 3181
QY 318 GGTGCTCCCTGCGCTTTGGCCATGTTCAATCTCAGAGAGATTACAGCGCTTCACACC 377
|||||
Db 3182 ggtgctccctgcccccttgccatgttcaattccagagaagattcagcgcttcacacc 3241
QY 378 TTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTTACTACTACATCTCGGTG 432
|||||
Db 3242 cttctccctcggtttgagttcttactctgagagacttactactactactctgtgag 3296

RESULT 9
US-09-442-366A-548
; Sequence 548, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashiev, Matvey E.
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-006CIP13
; CURRENT APPLICATION NUMBER: US/09/442.366A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 548
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-548
```

```
Query Match 42.0%; Score 267; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 CTGGGCTCAACGATTACATGACATTGTCTGCCCCCTACGAGGCCCGAGGCCGCCCT 228
|||||
Db 1 ctgggctcaacgattactactagacattgtctgccccctacgaagggccccct 60

QY 229 GAGGCCCCCGAGAGCTTTGCTTTGTACATGTGTGGACTGCCAGGCTATGAGTCCTGCCAG 288
|||||
Db 61 gagggccccgagacgtttgtctgtacatggtggactggccaggtatgagtcctgccag 120

QY 289 GCAGAGGCCCCCGGCTACAGCGCTGGGTGCTCTCCCTCTGGCCATGTTCAA 348
|||||
Db 121 gcagagggccccggcctacaagcgtgggtgtgctccctgcccccttggccatgtcaa 180

QY 349 TTCTCAGAGAGATTACAGCGTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACTCTGA 408
|||||
Db 181 ttctcagagaagattcagcgtctcacaccttctccctcggttggagttcttactctga 240

QY 409 GAGACTTACTACTACATCTCGGTGCC 435
|||||
Db 241 gagacttactactactctcgtgccc 267
```

```
RESULT 10
US-09-440-302B-242
; Sequence 242, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashiev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
```

```
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION NUMBER: US/09/440.302B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 242
LENGTH: 267
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302B-242

Query Match 42.0%; Score 267; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 CTGGGCTCAACGATTACATGACATTGTCTGCCCCCTACGAGGCCCGAGGCCGCCCT 228
|||||
Db 1 ctgggctcaacgattactactagacattgtctgccccctacgaagggccccct 60

QY 229 GAGGCCCCCGAGAGCTTTGCTTTGTACATGTGTGGACTGCCAGGCTATGAGTCCTGCCAG 288
|||||
Db 61 gagggccccgagacgtttgtctgtacatggtggactggccaggtatgagtcctgccag 120

QY 289 GCAGAGGCCCCCGGCTACAGCGCTGGGTGCTCTCCCTCTGGCCATGTTCAA 348
|||||
Db 121 gcagagggccccggcctacaagcgtgggtgtgctccctgcccccttggccatgtcaa 180

QY 349 TTCTCAGAGAGATTACAGCGTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACTCTGA 408
|||||
Db 181 ttctcagagaagattcagcgtctcacaccttctccctcggttggagttcttactctga 240

QY 409 GAGACTTACTACTACATCTCGGTGCC 435
|||||
Db 241 gagacttactactactctcgtgccc 267
```

```
RESULT 11
US-10-027-632-32020
; Sequence 32020, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32020
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-32020
```

```
Query Match      22.5%; Score 143.4; DB 7; Length 771;
Best Local Similarity 99.3%; Pred. No. 1.2e-24;
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCACAGACCAACCGGACCTCGGGGGGCGATCGCGCTGCTGCGGACTGTGCTC 60
Db 398 gccagcccaaacggacctcgggcgatgcggtgctgctgccccctgtgcgagctgctc 457
QY 61 TGGCGCGCGTTCCTCGGCTCCCTCTGCGGGGGGTCCAGCGTCCGCCACGAGTCTAC 120
Db 458 tgggcccgcgtcttcctcggtccctctgcgcgggggtccagctccgcacgtagctac 517
QY 121 TGGAACTCCAGTAACCCAGGTTGC 145
Db 518 tggaaactccagtaaacccaggtagc 542

RESULT 12
PCT-US02-25766-6624
; Sequence 6624, Application PC/TUS0225766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MONGER, William E
; APPLICANT: FAULK, Ronald
; APPLICANT: SUN, Hongwei
; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-WO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/311,837
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 13946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6624
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U14187
PCT-US02-25766-6624

Query Match      16.3%; Score 103.4; DB 1; Length 987;
Best Local Similarity 54.3%; Pred. No. 4.1e-15;
Matches 271; Conservative 0; Mismatches 201; Indels 27; Gaps 2;

QY 15 GACCTCGGGGGCGATCGGCTGCTGCCCTGCTGCGGACTGTCTCTGGGCCCGCTTCT 74
Db 60 ggcggcgctcctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 119
QY 75 CGGCTCCCTCTCGCGGGGGTCCAGCTCCGCCACGAGTAGTCTACTGGAACTCCAGTAA 134
Db 120 ggcaccaaggccgagggcgctggtgaaacccgcgcgtgctgactggaacagctccaa 179
QY 135 CCCAGGTTGCTTCAGGAGACCCGCTGTGGAGCTGGGCTCAACGATTACCTAGACAT 194
Db 180 ccagcaccctgcggcgagagggctacaccgtgcagggtgaaacgtaacgactatctgatat 239
QY 195 TGCTGCCCCCACTACGAAGGC-----CCAGGGGCCCTCTGA 230
Db 240 ttactgccgcactacaacagctcgggggtggcccccggggcgagccggcgaggg 299
QY 231 GGGCCCCGAGACGTTTGTGCTTTGTACATGTGTGACTGGCCAGGCTATGAGTCTGCCAGGC 290
Db 300 cggggcagagcagtagctgctgacatggtgagccgcaacgcgtaccgcacctgcaacgc 359
QY 291 ---AGAGGGCCCCCGGCGCTACAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATTTCA 347
Db 360 cagccagggtctcaagcgtggagtgcaacccggcgaccccgcaacgccccatcaa 419
QY 348 ATTCTCAGAGAAATTCAGCGCTTCACGCTTTTCTCCCTCGGCTTTTGTAGTTCTTACCTGG 407
Db 420 gttctcgagagaagttccacgcgtacacgccttctctctctggtctagagttccacgcgg 479
QY 408 AGAGACTTACTACTACATCTCGGTGCCACTCCAGAGAGTTCTTGGCCAGTGTCTGAGGCT 467
Db 480 ccacgagtagtactactatctccacgccccactcaaacctgcactggaagtgtctgagat 539
QY 468 CCAGGTGTCTGTCTGCTGC 486
Db 540 gaagggtctgtctgtgc 558

PCT-US02-25766-6624
; Sequence 6624, Application PC/TUS0225766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MONGER, William E
; APPLICANT: FAULK, Ronald
; APPLICANT: SUN, Hongwei
; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-WO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/311,837
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 13946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6624
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U14187
PCT-US02-25766-6624
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QY 348 ATTCTCAGAGAAATTCAGCGCTTCACGCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
Db 420 gttctcgagagaagttccacgcgtacacgccttctctctctggtctagagttccacgcgg 479
QY 408 AGAGACTTACTACTACATCTCGGTGCCACTCCAGAGAGTTCTTGGCCAGTGTCTGAGGCT 467
Db 480 ccacgagtagtactactatctccacgccccactcaaacctgcactggaagtgtctgagat 539
QY 468 CCAGGTGTCTGTCTGCTGC 486
Db 540 gaagggtctgtctgtgc 558

RESULT 13
US-09-053-375B-186
; Sequence 186, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-186

Query Match      16.3%; Score 103.4; DB 5; Length 987;
Best Local Similarity 54.3%; Pred. No. 4.1e-15;
Matches 271; Conservative 0; Mismatches 201; Indels 27; Gaps 2;

QY 15 GACCTCGGGGGCGATCGGCTGCTGCCCTGCTGCGGACTGTCTCTGGGCCCGCTTCT 74
Db 60 ggcggcgctcctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 119
QY 75 CGGCTCCCTCTCGCGGGGGTCCAGCTCCGCCACGAGTAGTCTACTGGAACTCCAGTAA 134
Db 120 ggcaccaaggccgagggcgctggtgaaacccgcgcgtgctgactggaacagctccaa 179
QY 135 CCCAGGTTGCTTCAGGAGACCCGCTGTGGAGCTGGGCTCAACGATTACCTAGACAT 194
Db 180 ccagcaccctgcggcgagagggctacaccgtgcagggtgaaacgtaacgactatctgatat 239
QY 195 TGCTGCCCCCACTACGAAGGC-----CCAGGGGCCCTCTGA 230
Db 240 ttactgccgcactacaacagctcgggggtggcccccggggcgagccggcgaggg 299
QY 231 GGGCCCCGAGACGTTTGTGCTTTGTACATGTGTGACTGGCCAGGCTATGAGTCTGCCAGGC 290
Db 300 cggggcagagcagtagctgctgacatggtgagccgcaacgcgtaccgcacctgcaacgc 359
QY 291 ---AGAGGGCCCCCGGCGCTACAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATTTCA 347
Db 360 cagccagggtctcaagcgtggagtgcaacccggcgaccccgcaacgccccatcaa 419
QY 348 ATTCTCAGAGAAATTCAGCGCTTCACGCTTTTCTCCCTCGGCTTTTGTAGTTCTTACCTGG 407
Db 420 gttctcgagagaagttccacgcgtacacgccttctctctctggtctagagttccacgcgg 479
QY 408 AGAGACTTACTACTACATCTCGGTGCCACTCCAGAGAGTTCTTGGCCAGTGTCTGAGGCT 467
Db 480 ccacgagtagtactactatctccacgccccactcaaacctgcactggaagtgtctgagat 539
QY 468 CCAGGTGTCTGTCTGCTGC 486
Db 540 gaagggtctgtctgtgc 558
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## RESULT 14

US-09-440-302B-838  
; Sequence 838. Application US/09440302B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Lukashov, Matvey E.  
; TITLE OF INVENTION: Human Neurobiology Array  
; FILE REFERENCE: CLON-006CIP11  
; CURRENT APPLICATION NUMBER: US/09/440,302B  
; CURRENT FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 1193  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 838  
; LENGTH: 987  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-440-302B-838

Query Match 16.3%; Score 103.4; DB 5; Length 987;

Best Local Similarity 54.3%; Pred. No. 4.1e-15;  
Matches 271; Conservative 0; Mismatches 201; Indels 27; Gaps 2;

```
QY 15 GACCTCGGGCGGATCGGCTGCTGCCCTGCTGCGGACTGCTCTCTGGCGCGCTCTCT 74
   || || || || || || || || || || || || || || || || || || || || ||
Db 60 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 119
   || || || || || || || || || || || || || || || || || || || || ||
QY 75 CGGCTCCCTCTCTCGCGGGGGCTCCACCTTCGCGCTGCGGAGCTGGGCTCAACGATTACCTAGACAT 134
   || || || || || || || || || || || || || || || || || || || || ||
Db 120 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 179
   || || || || || || || || || || || || || || || || || || || || ||
QY 135 CCCCAGGTTGCTTCGAGGAGACCCGCTGGTGGAGCTGGGCTCAACGATTACCTAGACAT 194
   || || || || || || || || || || || || || || || || || || || || ||
Db 180 ccagcaccctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 239
   || || || || || || || || || || || || || || || || || || || || ||
QY 195 TGCTCTCCCCCTACAGAGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 230
   || || || || || || || || || || || || || || || || || || || || ||
Db 240 ttactgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 299
   || || || || || || || || || || || || || || || || || || || || ||
QY 231 GGCCCGCGAGACCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCT 290
   || || || || || || || || || || || || || || || || || || || || ||
Db 300 cgggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 359
   || || || || || || || || || || || || || || || || || || || || ||
QY 291 ---AGAGGGCCCCCGGCTTACAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 347
   || || || || || || || || || || || || || || || || || || || || ||
Db 360 cagccggggcttcaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 419
   || || || || || || || || || || || || || || || || || || || || ||
QY 348 ATTCTCAGAGAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
   || || || || || || || || || || || || || || || || || || || || ||
Db 420 gtctcggagaagtccagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 479
   || || || || || || || || || || || || || || || || || || || || ||
QY 408 AGAGACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 467
   || || || || || || || || || || || || || || || || || || || || ||
Db 480 ccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 539
   || || || || || || || || || || || || || || || || || || || || ||
QY 468 CCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
   || || || || || || || || || || || || || || || || || || || || ||
Db 540 gaagggtgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 558
   || || || || || || || || || || || || || || || || || || || || ||
```

## RESULT 15

PCT-US02-13644-14  
; Sequence 14. Application PC/TUS0213644  
; GENERAL INFORMATION:  
; APPLICANT: Chien, Kenneth  
; APPLICANT: Hoshijima, Masahiko  
; TITLE OF INVENTION: Non-viral vesicle vector for cardiac specific gene delivery  
; FILE REFERENCE: 6627-PAL198  
; CURRENT APPLICATION NUMBER: PCT/US02/13644  
; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: 60/287,423  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 1480  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-13644-14

Query Match 16.0%; Score 101.8; DB 1; Length 1480;  
Best Local Similarity 56.9%; Pred. No. 1e-14;  
Matches 253; Conservative 0; Mismatches 177; Indels 15; Gaps 3;

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QY 56 TCCTCTGGGCGCGCTTCCTCGGCTCCCTCTGCGGGGGCTCCACGCTCCGCGCAGTAG 115
   || || || || || || || || || || || || || || || || || || || || ||
Db 81 tctctggggccctctctctctctctctctctctctctctctctctctctctctctctctct 140
   || || || || || || || || || || || || || || || || || || || || ||
QY 116 TCTACTGGAACTCCAGTAACCCGAGGTTGCTTCGAGGAGACGCGGTGGTGGAGCTGGGCC 175
   || || || || || || || || || || || || || || || || || || || || ||
Db 141 tctctgggaacagtccaatcccaagttccggaatgaggactacaccatacatgtgcagc 200
   || || || || || || || || || || || || || || || || || || || || ||
QY 176 TCAACGATTACCTAGACATGTGTCGCCCCACTACGAAAGG---CCAGGGCCCCCTGAGG 232
   || || || || || || || || || || || || || || || || || || || || ||
Db 201 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgtg 260
   || || || || || || || || || || || || || || || || || || || || ||
QY 233 GCCCCGAGAGACGTTGCTTTGTATCATGTGTGACTGGCCAGGCTATGATCTTGCAGGCAG 292
   || || || || || || || || || || || || || || || || || || || || ||
Db 261 ccattggagcagtcatactctgtacctggtggagcagtagaggtaccagctgtgccagcccc 320
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QY 293 AGGGCCCCCGGCTTACAAAGCGCTGGGTGTGCTTCCCTGCGCCTT-----TGGCCATG 343
   || || || || || || || || || || || || || || || || || || || || ||
Db 321 ag---tccaaggaccaagtcctgcagtcgcaacccgcccagtgccaagcatggcccg 377
   || || || || || || || || || || || || || || || || || || || || ||
QY 344 TTCATTTCTCAGAGAGATTACGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTAC 403
   || || || || || || || || || || || || || || || || || || || || ||
Db 378 agaagctgtctgagaagttccagcgttcacaccttcacctgggcaaggagttcaag 437
   || || || || || || || || || || || || || || || || || || || || ||
QY 404 CTGGAGAGACTTACTACTACTACTACTACTCTGGTGGCTCCCACTCCAGAGAGTTCTGGCCAGTGTGA 463
   || || || || || || || || || || || || || || || || || || || || ||
Db 438 aaggacacagctactactactactactctccaaacccatccaccagcatgaagaccgtctgttga 497
   || || || || || || || || || || || || || || || || || || || || ||
QY 464 GGCTCCAGGTGTGTGTCTGTCTGCA 488
   || || || || || || || || || || || || || || || || || || || || ||
Db 498 ggttgaaggtgactgctcagtggtgcaa 522
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Search completed: September 28, 2002, 01:35:28  
Job time: 12728 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 22:03:08 ; Search time 2180.79 Seconds  
(without alignments)  
3936.217 Million cell updates/sec

Title: US-09-904-954-3  
Perfect score: 636  
Sequence: 1 GCCAGACCAACCGACCTC.....TTCTGCCAATTCGTGTGAGCC 636

Scoring table: IDENTITY\_NUC  
Gap 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622.4	97.9	912	BI868252	BI868252 603392205
2	610.4	96.0	707	BE883793	BE883793 601506189
3	597	93.9	838	BE890843	BE890843 601431292
4	456.4	71.8	493	BI868252	BI868252 603392205
5	456.4	71.8	493	BI868252	BI868252 603392205
6	442.6	69.6	1255	AK012195	AK012195 Mus muscu
7	440.4	69.2	482	BI868252	BI868252 603392205
8	414.4	65.2	751	BE792518	BE792518 60253627
9	404.2	63.6	778	BE138971	BE138971 601784106
10	400.4	63.0	1054	BI868252	BI868252 603392205
11	399.4	62.8	561	AW784975	AW784975 115339 MA
12	396.6	62.4	542	BE750737	BE750737 202345 MA
13	392	61.6	554	BE236077	BE236077 143746 MA
14	384.8	60.5	963	BI868252	BI868252 603392205
15	378.8	59.6	565	BE032073	BE032073 130886 MA
16	365	57.4	375	AW405707	AW405707 UI-HF-BL0
17	359.2	56.5	567	BE899787	BE899787 182909 MA

18	356.8	56.1	544	9	AV608466
19	340.6	53.6	541	9	AI663168
20	327.8	51.5	464	9	AI664495
21	321	50.5	458	10	BF189993
22	311.4	49.0	469	9	AW741367
23	291.6	45.8	476	9	BE234774
24	274.4	43.1	837	10	BI258895
25	274.2	43.1	453	9	AA002297
26	253.4	39.8	409	9	AA289704
27	252	39.6	506	10	BF441035
28	250	39.3	870	10	BE780161
29	248	39.0	334	10	BF442110
30	242.2	38.1	298	10	BF224394
31	236.4	37.2	338	9	AW315678
32	231.2	36.4	482	10	BF441034
33	216.4	34.0	600	10	BI868340
34	211.6	33.3	353	9	AW462601
35	209.4	32.9	635	10	BI083742
36	199.4	31.4	442	9	AA015379
37	196	30.8	233	9	AA312329
38	188.4	29.6	373	9	AA003996
39	187.6	29.5	391	10	W12777
40	187.4	29.5	492	10	BM258125
41	181.2	28.5	530	10	BF470931
42	172.2	27.1	676	9	AL661297
43	171.2	26.9	179	9	AA296663
44	161.4	25.4	586	10	BJ074808
45	158.6	24.9	592	10	BJ031724

## ALIGNMENTS

RESULT 1  
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LOCUS 603392205F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:5402208 5',  
DEFINITION mRNA sequence.  
ACCESSION BI868252  
VERSION BI868252.1 GI:16041925  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 912)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM12025 row: j column: 01  
High quality sequence stop: 806.  
Location/Qualifiers  
1. 912  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5402208"  
/clone\_lib="NIH\_MGC\_90"  
/tissue\_type="adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: liver; Vector: PCMV-SPORT6; Site:1: NotI;  
Site:2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.7 Kb. Library enriched for full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

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BASE COUNT      175 a      282 c      264 g      191 t
ORIGIN

Query Match      97.9%; Score 622.4; DB 10; Length 912;
Best Local Similarity 99.7%; Pred. No. 9.9e-137;
Matches 634; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCCAGACCAACCGGACCTCGGGGGCGATCGGGTGTGCTGCCCTGTGCTGCGGACTGTGCTC 60
DB 12 GCCAGACCAACCGGACCTCGGGGGCGATCGGGTGTGCTGCCCTGTGCTGCGGACTGTGCTC 71

QY 61 TGGGCCCGCTTCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCCGCCACGAGTAGTCTAC 120
DB 72 TGGGCCCGCTTCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCCGCCACGAGTAGTCTAC 131

QY 121 TGGAACTCCAGTAAACCCAGTGTCTTCGAGGAGACGCCGTGTGGAGCTGGGCCCTCAAC 180
DB 132 TGGAACTCCAGTAAACCCAGTGTCTTCGAGGAGACGCCGTGTGGAGCTGGGCCCTCAAC 191

QY 181 GATTACCTAGACATTTGTCTGCCCCACTACGAAGGCCCGAGGGCCCCCTGAGGGCCCCGAG 240
DB 192 GATTACCTAGACATTTGTCTGCCCCACTACGAAGGCCCA-GGCCCCCTGAGGGCCCCGAG 250

QY 241 ACGTTTCTTGTACATGGTGGACTGCCAGGCTATGAGTCTGCCAGGCGAGGGCCCC 300
DB 251 ACGTTTCTTGTACATGGTGGACTGCCAGGCTATGAGTCTGCCAGGCGAGGGCCCC 310

QY 301 CGGGCTTACAAAGCGCTGGGTGTGCTCCCTGCCCTTGGCCATGTTCAATTTCTCAGAGAAG 360
DB 311 CGGGCTTACAAAGCGCTGGGTGTGCTCCCTGCCCTTGGCCATGTTCAATTTCTCAGAGAAG 370

QY 361 ATTACGCGCTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
DB 371 ATTACGCGCTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 430

QY 421 TACATCTCGTGCCCACTCCAGAGATTCTGGCCAGTGTCTGAGGCTCCAGGCTGTCTGTC 480
DB 431 TACATCTCGTGCCCACTCCAGAGATTCTGGCCAGTGTCTGAGGCTCCAGGCTGTCTGTC 490

QY 481 TGCTGAAGGAGAGAGAGTCTGAGTCAAGCCATCTCTTGGGAGCCCTCGAGAGAGTGGC 540
DB 491 TGCTGAAGGAGAGAGAGTCTGAGTCAAGCCATCTCTTGGGAGCCCTCGAGAGAGTGGC 550

QY 541 ACATCAGGCTGGGAGGGGGACACTCCAGGCCCTCTGCTCTTGTCTTACTTACTGCTG 600
DB 551 ACATCAGGCTGGGAGGGGGACACTCCAGGCCCTCTGCTCTTGTCTTACTTACTGCTG 610

QY 601 CTCTGTGATTTCTGCTCTTCTGCGAATTTCTGTAGCC 636
DB 611 CTCTGTGATTTCTGCTCTTCTGCGAATTTCTGTAGCC 646

RESULT 2
BE883793
LOCUS      707 bp mRNA linear EST 20-OCT-2000
DEFINITION 601506189F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907510 5',
            mRNA sequence.
ACCESSION  BE883793
VERSION    BE883793.1 GI:10332569
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 707)
REFERENCE  NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ARCC
            CDNA Library Preparation: Life Technologies, Inc.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9718 row: b column: 23
High quality sequence stop: 706.

FEATURES
    source              1..707
    Location/Qualifiers
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:3907510"
        /lab_host="DH10B (phage-resistant)"
        /tissue_type="leiomyosarcoma"
        /note="Organ: uterus; Vector: pCMV-SPORT6; Site.1: Noti;
        Site.2: Sali; Cloned unidirectionally. Primer: Oligo dt.
        Average insert size 2.1 kb."
    BASE COUNT      119 a      228 c      204 g      156 t
    ORIGIN

Query Match      96.0%; Score 610.4; DB 10; Length 707;
Best Local Similarity 99.5%; Pred. No. 6.2e-134;
Matches 633; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 GCCAGACCAACCGGACCTCGGGGGCGATCGGGTGTGCTGCCCTGTGCTGCGGACTGTGCTC 60
DB 22 GCCAGACCAACCGGACCTCGGGGGCGATCGGGTGTGCTGCCCTGTGCTGCGGACTGTGCTC 81

QY 61 TGGGCCCGCTTCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCCGCCACGAGTAGTCTAC 120
DB 82 TGGGCCCGCTTCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCCGCCACGAGTAGTCTAC 141

QY 121 TGGAACTCCAGTAAACCCAGTGTCTTCGAGGAGACGCCGTGTGGAGCTGGGCCCTCAAC 180
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QY 181 GATTACCTAGACATTTGTCTGCCCCCACTACGAAGGCCCGAGGGCCCCCTGAGGGCCCCGAG 240
DB 202 GATTACCTAGACATTTGTCTGCCCCCACTACGAAGGCCCA-GGCCCCCTGAGGGCCCCGAG 260

QY 241 ACGTTTCTTGTACATGGTGGACTGCCAGGCTATGAGTCTGCCAGGCGAGGGCCCC 300
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ACCESSION BE890843  
VERSION BE890843.1 GI:10349570  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 838)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9741 row: h column: 24  
High quality sequence stop: 707.  
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/lab\_host="DH10B (phage-resistant)"  
/note="organ: skin; Vector: PCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 2 kb. Library constructed by Life  
Technologies."  
BASE COUNT 135 a 265 c 256 g 182 t  
ORIGIN  
Query Match 93.9%; Score 597; DB 10; Length 838;  
Best Local Similarity 98.1%; Pred. No. 9.6e-131;  
Matches 625; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
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QY 61 TGGGCGCGCTTCTCGGCTCCCTCTCGCGGGGGCTCCAGCTCCGCCACGTAAGTCTAC 120  
DB 104 TGGGCGCGCTTCTCGGCTCCCTCTCGCGGGGGCTCCAGCTCCGCCACGTAAGTCTAC 163  
QY 121 TGAACCTCAGTAACCCCGAGTGTCTTCGAGGAGAGCCGCTGGTGGAGTGGGCGCTCAAC 180  
DB 164 TGAACCTCAGTAACCCCGAGTGTCTTCGAGGAGAGCCGCTGGTGGAGTGGGCGCTCAAC 223  
QY 181 GATTACTAGACATTTCTGCCCCCACTAGCAAGGCCAGGGCCCCCTGAGGGCCCCGAG 240  
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QY 541 ACATCAGGTTGGCGA-GGGGGGACACTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 599  
DB 583 ACATCAGGTTGGCGA-GGGGGGACACTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 642  
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mRNA sequence.  
ACCESSION BG747752  
VERSION BG747752.1 GI:14058405  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 493)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM1675 row: 1 column: 12  
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/note="organ: eye; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into ECORI/XhoI sites using the following 5',  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library.!"  
BASE COUNT 79 a 167 c 144 g 103 t  
ORIGIN  
Query Match 71.8%; Score 456.4; DB 10; Length 493;  
Best Local Similarity 99.8%; Pred. No. 1.2e-97;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCCAGACCAACCGGACCTCGGGGGGATCGCGCTCTGCCCTCTGTCGGGACTGTCTTC 60  
DB 36 GCCAGACCAACCGGACCTCGGGGGGATCGCGCTCTGCCCTCTGTCGGGACTGTCTTC 95  
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Db 96 TGGGCCGGTTCCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 155
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RESULT 5
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DEFINITION 602706466F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842977 5',
mRNA sequence.
ACCESSION BG748489
VERSION BG748489.1 GI:14059142
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 495)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1678 row: d column: 18
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/Note="Organ: eye; Vector: pORF7; site_1: XhoI; site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library. |"
79 a 168 c 144 g 104 t
BASE COUNT
ORIGIN
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Query Match 71.8%; Score 456.4; DB 10; Length 495;  
Best Local Similarity 99.8%; Pred. No. 1.2e-97;  
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GCAGAGCAAAACCGACCTCGGGGGGATCGCGCTGCTGCCCTTGTGCGGAGTGTCTC 60
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Qy 241 ACGTTTCTTTGATACATTTGGTGGACTGCCAGGCTATGAGTCTGCCAGGAGGGCCCC 300
Db 278 ACGTTTCTTTGATACATTTGGTGGACTGCCAGGCTATGAGTCTGCCAGGAGGGCCCC 337
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Db 398 ATTACGCGCTTACACCTTTCTCCCTCGGCTTTGAGTCTTACCTGGAGAGACTTACTAC 457
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Db 458 TACATCTCGTGCCCACTCCAGAGAGTTCTGGCCAGTG 495
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RESULT 6

LOCUS AK012195  
DEFINITION AK012195 1255 bp mRNA linear HTC 19-JAN-2002  
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length  
enriched library, clone:2610529M21:ephra A4, full insert sequence.  
ACCESSION AK012195  
VERSION AK012195.1 GI:12848791  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA,  
clone:2610529M21.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (sites)  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE 2 (sites)

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159

REFERENCE 3 (sites)

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5 (bases 1 to 1255)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imocani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriber, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Soabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyota, T., Yamamura, T., Yamashita, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

## Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

## Location/Qualifiers

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Matches 537; Conservative 0; Mismatches 99; Indels 15; Gaps 2;

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Db 176 TGGAACTCCAGTAACCCAGGTTGCTTCAGGAGATGCCGTGGAGCTGGGCTCAAC 235  
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Db 296 ACCTTTGCATTATACATCGTGGAGCTGGTCAAGGCTACGAGGCTTCGAGGAGGAGG 355  
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Db 596 COTGAGAAAGCGGTACGTCGGGTGGCGGGGAGGACACGCGCCAGCCCCCTGTGTCTC 655  
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## RESULT 7

## BG338638

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

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REFERENCE 1 (bases 1 to 778)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapb-r@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LAM9252 row: k column: 02  
High quality sequence stop: 667.  
Low quality sequence stop: 778.

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BASE COUNT 143 a 235 c 239 g 161 t

ORIGIN

Query Match 63.6%; Score 404.2; DB 10; Length 778;  
Best Local Similarity 83.3%; Pred. No. 3.1e-85;  
Matches 499; Conservative 0; Mismatches 88; Indels 12; Gaps 3;

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DB 74 TGGGCGGCTGCTCGGCTCGCGCTCGCGGGTCTCCAGCTCGGCGACCAATCTAC 133  
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QY 301 CGGGCTACAGCGTGGTGTGCTCCCTGCGCTTG-----GCCATGTTCAATC 351  
DB 314 AATGCTTCCAGCGTGGAAATGCTCGATGCTTTTGGCCCTTTTCAGGCTTTGATTC 373  
QY 352 TCAGAGAGATTTCAGCGCTTCACACTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAG 411  
DB 374 TCAGAAAGATTTCAGCGCTTACACCTTCCCGCTGGGCTTTGAGTTCTTGGCTGGAGAG 433  
QY 412 ACTTACTACTACATCTCGGTGCCACTCCAGAGAGTTCTGGCCAGTGTGAGGCTCCAG 471  
DB 434 ACTTACTACTACATCTCGGTGCCAGTCCCGAGAGTCTCGGCGGTGCTGAGACTCCAG 493  
QY 472 GTGTCTGTCTGCAAGGAGAGAGTCTGAGTCAAGCCCTCTGTTGGGAGCCCTGGA 531  
DB 494 GTGTCTGTCTGCAAGGAGAGCGGTCGGAGTCAGCTCATCTCTGTTGGGAGTCTGGA 553

QY 532 GAGAGTGCACATCAGGTGCGAGGGGGGAGACTCCAGCCCTCTGTCTCTTGTCT 590  
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RESULT 10  
BI663095 1054 bp mRNA linear EST 12-SEP-2001  
LOCUS 603286494F1 NCI-CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5320846 5',  
DEFINITION mRNA sequence.  
ACCESSION BI663095  
VERSION BI663095.1 GI:15577328  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Location/Qualifiers  
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/strain="FVB/N"  
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/clone\_lib="IMAGE:5320846"  
/clone\_lib="NCI-CGAP\_Mam6"  
/sex="female, virgin"  
/tissue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 208 a 333 c 322 g 191 t

ORIGIN

Query Match 63.0%; Score 400.4; DB 10; Length 1054;  
Best Local Similarity 82.4%; Pred. No. 2.7e-84;  
Matches 537; Conservative 0; Mismatches 96; Indels 19; Gaps 6;

QY 1 GCCAGACCAACCGGACCTCGGGCGGATGCGGCTGCTGCCCTCTGCGGACTGTCTCTC 60  
DB 25 GCAGACCAAGATGGACC-CCAGGGCGATGCGGCTGCTGCCCTCTGCGGACTGTCTC 83  
QY 61 TGGGCGGCTTCTCGGCTCCCTCTTCGCGGGGGCTCCAGCTCGGCGACCTAGTCTAC 120  
DB 84 TGGGCGGCTGCTCGGCTCGGCTCGGCGGCTGCTCCAGCTCGGCGACCAATCTAC 143  
QY 121 TGGAACTCCAGTAACCCAGGTTGCTTCAGGAGAGCGGCTGGTGGAGCTGGGCTCAAC 180  
DB 144 TGGAACTCTTAACCCCGGAGTTGCTTCAGGAGAGTGGCTGGTGGAGCTGGGCTTCAAC 203  
QY 181 GATTACCTAGACATTTCTGCCCCACCTACGAAGGCCCGCCCTCAGGGCCCGGAG 240  
DB 204 GATTACCTAGACATTTCTGCCACATTAAGAGCCCA--GGCCCCCAGAGGCCCGGA 262  
QY 241 AGTTTGTCTTGTACATGTGAGTGGGCTATGAGTCTCTGCGAGGAGGAGGCC 300

Db 263 ACCTTTGCATTATACATGGTGGACTGGCTAGGCTACGAGCCCTCCACGGCAGAGGGGCA 322  
QY 301 CGGCGCTACAGCGCTGGGTGGTCTCCCTCCCTCTTG-----GCCATGTTCAATTC 351  
Db 323 ANTGCCTTCCAGCGCTGGAAATGCTTCGATGCCCTTTTGCCTCTTTCAGCCCTGTTCGATTC 382  
QY 352 TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTTGGTCTTTACCTGGAGAG 411  
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QY 412 ACTTACTACTACATCTCGGTGCCCTCCAGAGAGTTCTGGCAGAGTCTGGAGGCTCCAG 471  
Db 443 ACTTACTACTACATCTCGGTGCCCTCCAGAGAGTCTCGGCGGTGCTTGAGAGTCCAG 502  
QY 472 GTGCTCTGCTGCTGCAAGGAGAGAGTCT-----TGAGTCAGCCATCTGTTGGGAGC 525  
Db 503 GTGCTGCTGCTGCAAGGAGAGAGGCTCATCATGATGATGATCATCTGTTGGAGT 562  
QY 526 CTTGGAGAGAGTGGACATCAGGCTGGCGAGGGGGGACACTCCAGCCCTCTGCTCTC 585  
Db 563 CTTGGAGAGAGGCTGCTCGGTGGCGGAGGAGACACGCGCCAG-CCCTGTGTGCTC 621  
QY 586 TTGCTATTACTGCTGCTGATCTTCG--TCTTCTGCGAATCTGTGAGCC 636  
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RESULT 11  
AW784975  
LOCUS AW784975 561 bp mRNA linear EST 09-JUL-2000  
DEFINITION 115339 MARC 1P1G Sus scrofa cdna 5', mRNA sequence.  
ACCESSION AW784975  
VERSION AW784975.1 GI:7841751  
KEYWORDS EST.  
SOURCE Pig.  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 561)  
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,  
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.  
and Keele, J.W.  
Design and use of two pooled tissue normalized cdna libraries for  
EST discovery in swine  
Unpublished (2000)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCCAGTCAGAGC  
Plate: 48 row: C column: 4  
Seq primer: ATTTAGGTGACACTATAG.  
Location/Qualifiers  
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/clone\_lib="MARC 1P1G"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from day 11, 13, 15, 20,  
and 30 embryos."  
93 a 181 c 174 g 113 t

FEATURES  
source

BASE COUNT 93 a 181 c 174 g 113 t  
ORIGIN

Query Match 62.8%; Score 399.4; DB 9; Length 561;  
Best Local Similarity 87.5%; Pred. No. 3.8e-84;  
Matches 463; Conservative 0; Mismatches 56; Indels 10; Gaps 2;  
QY 1 GCAGAGCAAAACCGGACCTCGGGGGGATGCGGCTGCTGCCCTGCTGCGGAGATGCTCTC 60  
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QY 61 TGGCGCGGCTTCTCGGCTCCCTCTCGCGGGGGCTCCAGCCTCGGCCACGTAGTCTAC 120  
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QY 121 TGGAACTCCAGTAACCCAGGTTGCTTCGAGGAGAGCCCTGCTGGAGTCTGGGCTCAAC 180  
Db 153 TGGAACTCCAGTAACCCAGGCTGCTTCGAGGAGAGCCGCTGCTGGAGCTGGGCTCAAG 212  
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QY 241 ACCTTTGCTTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
Db 273 ACCTTTGCTTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 332  
QY 301 CGGCGCTTACAGCGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351  
Db 333 GGTGCTTCAAGCGCTGGGAGTGTCTCCCGCCCTTTGCTGCTGCTGCTGCTGCTGCTGCT 392  
QY 352 TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTCTTACCTGAGAG 411  
Db 393 TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTCGAGTCTTGTGCTGAGAG 452  
QY 412 ACTTACTACTACATCTCGGTGCCACTCC--AGAGAGTCTTGGCCAGTCTGTTGAGGCTCCA 470  
Db 453 ACCTACTACTACATCTCAGTGCCCACTCCGGGAGAGTCTCGGCCAGTCTGTTGAGGCTCCA 512  
QY 471 GGTGCTGCTGCTGCTCAAGGAGAGAGTCTGAGTCCAGCCCATCTCTGTT 519  
Db 513 GGTGCTGCTGCTGCTCAAGGAGAGAGTCTGAGTCCAGCCCATCTCTGTT 561

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DEFINITION 202345 MARC 4BOV Bos taurus cdna 5', mRNA sequence.  
ACCESSION BE750737  
VERSION BE750737.1 GI:10164729  
KEYWORDS EST.  
SOURCE COW.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 542)  
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,  
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,  
Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and  
Keele, J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cdna  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)  
21180013  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.  
PCR Primers

TITLE  
JOURNAL  
MEDLINE  
COMMENT

FORWARD: AGGAAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGCTCAGCAGG  
Plate: 113 row: B column: 13  
Seq primer: ATTAGTGACACTATAG.  
Location/Qualifiers

## FEATURES

source

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/tissue\_type="pooled"  
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/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from day 20 and day 40  
embryos."

BASE COUNT 94 a 177 c 161 g 110 t

## ORIGIN

Query Match 62.4%; Score 396.6; DB 10; Length 542;  
Best Local Similarity 85.4%; Pred. No. 1.7e-83;  
Matches 457; Conservative 0; Mismatches 69; Indels 9; Gaps 1;

Qy 1 GCAGACCAACCGGACCTCGGGGGGATGCGGCTGCTGCCCTGCTCGGACTGTCCTC 60  
Db 7 GCAGACCAACCGGACCTCGGGGGGATGCGGCTGCTGCCCTGCTCGGACTGTCCTC 66  
Qy 61 TGGGCGCGCTTCTCGGCTCCCTCTGCGCGGGGCTCCAGCCTCGGCCACCTAGTCTAC 120  
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Qy 121 TGAACCTCAGTAACCCAGGTTGCTTCGAGGAGACGCGGTGGAGTGGGCTCAAC 180  
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Db 307 AGTGCTTCAAGCGTGGGAGTGTCCCGCCCTTCGCTCCCTTTGGCCCTGTTGATTT 366  
Qy 352 TCAGAGAGATTCAGGCTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACTCGAGAG 411  
Db 367 CCAGAGAGATTCAGGCTTACACCTTTCTCCCTTGGCATGGAGTTCTTGGCGGAGAG 426  
Qy 412 ACTTACTACTATCTCGGTGCGGCTCCAGAGAGTCTTGGCGAGTGTGAGGCTCCAG 471  
Db 427 ACTTACTACTATCTCAGTGCACCTCGGGAGTCTTGGCGAGTGTGAGGCTCCAG 486  
Qy 472 GTGCTGTGCTGCAAGGAGGAGAGTGTGAGTCAAGCCATCTCTTTGGGAGCC 526  
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## RESULT 13

BE236077

LOCUS BE236077 554 bp mRNA linear EST 10-JUL-2000  
DEFINITION 143746 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BE236077

VERSION BE236077.1 GI:9020795

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

1 (bases 1 to 554)

Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,

Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.

## TITLE

## JOURNAL

## COMMENT

and Keele, J.W.  
Design and use of two pooled tissue normalized cDNA libraries for  
EST discovery in swine  
Unpublished (2000)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@mail.marc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.

## PCR Primers

FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGCTCAGCAGG

Plate: 85 row: N column: 6

Seq primer: ATTAGTGACACTATAG.

## FEATURES

source

Location/Qualifiers

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/clone\_lib="MARC 1P1G"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from day 11, 13, 15, 20,  
and 30 embryos."

BASE COUNT 92 a 181 c 171 g 110 t

## ORIGIN

Query Match 61.6%; Score 392; DB 9; Length 554;  
Best Local Similarity 87.2%; Pred. No. 2.1e-82;  
Matches 457; Conservative 0; Mismatches 55; Indels 12; Gaps 2;

Qy 1 GCAGACCAACCGGACCTCGGGGGGATGCGGCTGCTGCCCTGCTCGGACTGTCCTC 60  
Db 34 GCAGACTAACACGACGCGGGGGGATGCGGCTGCGGCTGCTCGGACTGTCCTC 93  
Qy 61 TGGGCGCGCTTCTCGGCTCCCTCTGCGCGGGGCTCCAGCCTCGGCGGCTGCTAC 120  
Db 94 TGGGCGCGCTTCTCGGCTCCCTCTGAGAGGAGCTCTGGTCTCGGCGGCTGCTAT 153  
Qy 121 TGAACCTCAGTAACCCAGGTTGCTTCGAGGAGACGCGGTGGAGTGGGCTCAAC 180  
Db 154 TGAACCTCAGTAACCCAGGTTGCTTCGAGGAGACGCGGTGGAGTGGGCTCAAG 213  
Qy 181 GATTACCTAGACATTTCTGCCCCCCTACGAGGCGGCGGCTCGGCGGCGGCGG 240  
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Qy 241 AGTTTGTCTTACATGTGAGTGGCGGCTGAGTCTTCCAGGAGGAGGCGGCGG 300  
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Qy 352 TCAGAGAGATTCAGCGCTTACACCTTTCTCCCTCGGCTTTGAGTTCTTACTGGAGAG 411  
Db 394 TCAGAGAGATTCAGCGCTTACACCTTCTCCCTGGGCTTCGAGTTCTTGGCTGGAGAG 453  
Qy 412 ACTTACTACTATCTCGGTCGCCCTCAGAGAGTTCGCGGAGTGTGAGGCTGAGGCTCCAG 471  
Db 454 ACCTACTACTACTCT---TGCCAACTCGGAGAGTCTTGGCGGCTGCTTGGGCTCCAG 510  
Qy 472 GTGCTGTGCTGCAAGGAGGAGAGTCTGAGTCAGGCCCATCC 515  
Db 511 GTGCTGTGCTGCAAGGAGGAGGAGGCTGAGTCGGGCCCATCC 554



[illegible]



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Db 75 GGCTGCTTCGAGAGAGCGCGTGGTGGAGCTGGGCGCTCAAGGATTACCTAGACATCTTCT 134
QY 200 GCGCCCACTACGAAGCGCCCTGAGGGCCCGGAGAGCGTTTGTGTGTACATGG 259
Db 135 GCGCCCACTATGAGAGCGCCCGGAGAGCGTTTGTGTGTATACATGG 194
QY 260 TGGACTGGCCAGGCTATGAGTCTGCCAGGCGAGAGGGCCCGGGCTTACAAGCGCTGGG 319
Db 195 TGGACTGGTGGGCTATGAGGCGTGCAGGCGGAGGGCCAGGTGCCTTCAAGCGCTGGG 254
QY 320 TGTGCTCCC-----TGCCTTTGGCCATGTTCAATTCAGAGAGATTCAGCGCT 370
Db 255 AGTGTCCCGCCCGCTTTGCTCCCTTTGGCCCTGTGGCGATTCTCAGAGAGATTCAGCGCT 314
QY 371 TCACACCTTCTCCCTCGGCTTTGAGTCTTACCTGGAGAGACTTACTACTACATCTCGG 430
Db 315 TCACACCTTCTCCCTGGGCTTCGAGTCTTGGCTGGAGAGCTTACTACTACATCTCAG 374
QY 431 TGCCCACTCCAGAGAGTTCTGGCCAGTGTGTGAGGCTCCAGGTGTCTGTGTGCAAGG 490
Db 375 TGCCCACTCCGAGAGTCTCTGGCCAGTGTGTGAGGCTCCAGGTGTCTGTGTGCAAGG 434
QY 491 AGAGGAAGTCTGAGTCAGCCCATCTCTGTTGGGAGCCCTGGAGAGCTGGCAGATCAGGGT 550
Db 435 AGGACAAGCCTGAGTCGGGCCCATCTCTGTTGGGAGCCCTGGAGAGCTGGCAGCTCAGGT 494
QY 551 GGGAGGGGGGAGACTCCAGCCCTCTGTCTCTTGTCTTATTTACTGCTGCTTCTGATTC 610
Db 495 GGCAGGGGGGGGCGCACTCCAGCCCTCTGTCTCTTGTCTCTGTCTGTCTGTCTGTCTG 554
QY 611 TTCGCTCTTCT 620
Db 555 TGCCTCTCCT 564

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2002, 01:36:51 ; Search time 74.08 Seconds  
(without alignments)  
301.375 Million cell updates/sec

Title: US-09-904-954-4  
Perfect score: 1091  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	1091	100.0	201	Human hek-L protei
2	380.5	34.9	228	Human AL-1, a liga
3	380.5	34.9	228	Lerk-7 protein. H
4	380.5	34.9	228	HEK4 binding prote
5	380.5	34.9	335	Novel human diagno
6	366.5	33.6	234	Eph transmembrane
7	364.5	33.4	238	Human hek-L protei
8	359	32.9	200	Chicken Eph recept
9	359	32.9	200	Amino acid sequenc
10	343	31.4	204	Human PRO202 polyp
11	343	31.4	204	Human PRO202 prote

12	342.5	31.4	209	17	AAR94766	Mouse Eph receptor
13	342.5	31.4	209	19	AAW71006	Amino acid sequenc
14	340.5	31.2	213	20	AAW06822	Human LERK-6 polyp
15	335.5	30.8	205	22	AAB50990	Human PRO202 prote
16	335.5	30.8	218	21	AAB54058	Human pancreatic c
17	334.5	30.7	205	13	AAR23895	B61 protein sequen
18	334.5	30.7	205	15	AAR53634	EBP. Homo sapiens
19	334.5	30.7	205	16	AAR82604	Eph transmembrane
20	334.5	30.7	205	18	AAW04632	ek receptor bindi
21	330.5	30.3	184	17	AAW02587	Lerk-6 protein. M
22	330.5	30.3	184	17	AAR91283	Lerk-6 protein. M
23	330.5	30.3	184	20	AAW06820	Murine LERK-6 poly
24	313.5	28.7	151	18	AAW18078	Truncated eck rece
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29	308	28.2	179	17	AAR94768	Eph receptor ligand
30	308	28.2	179	19	AAW71008	Generic sequence f
31	261.5	24.0	104	17	AAR91284	LERK-6 exon polytpe
32	261.5	24.0	104	20	AAW06821	Amino acid sequenc
33	169.5	15.5	340	18	AAW33699	Human cytokine Ler
34	169.5	15.5	340	18	AAW31544	AL-2-short (AL-2s)
35	169.5	15.5	340	18	AAW10637	Human family ligand
36	169.5	15.5	340	18	AAW17081	Human transmembran
37	169.5	15.5	340	19	AAW46615	AL-2-long (AL-2l)
38	169.5	15.5	455	18	AAW33698	Chicken Eph recept
39	166.5	15.3	331	17	AAW00288	Ephrin-B2-Ephrin-B
40	166	15.2	658	21	AAW96782	Mouse Eph receptor
41	164.5	15.1	334	17	AAW00287	Murine hepatoma tr
42	164.5	15.1	336	17	AAR92742	Drosophila melanog
43	158.5	14.5	652	22	ABB58621	Drosophila melanog
44	158.5	14.5	652	22	ABB65548	Full length ligand
45	156	14.3	333	17	AAW06337	

ALIGNMENTS

RESULT 1			
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XX	AC	AAW71482;	
XX	DT	03-OCT-1995 (first entry)	
XX	DE	Human hek-L protein.	
XX	KW	Ligand; cell surface; tyrosine kinase receptor; tumorigenesis; immunogen.	
XX	OS	Homo sapiens.	
XX	XX	Key	Location/Qualifiers
FT	Peptide	1..22	/note= "signal peptide"
FT	Protein	23..201	
XX	PN	WO9506065-A.	
XX	PD	02-MAR-1995.	
XX	PF	17-AUG-1994;	94WO-US09282.
XX	PR	20-AUG-1993;	93US-0109745.
XX	PR	30-AUG-1993;	93US-0114426.
XX	PR	03-DEC-1993;	93US-0161132.
XX	PR	09-MAY-1994;	94US-0240124.
XX	PA	(IMV ) IMMUNEX CORP.	
XX	PI	Beckmann MP, Cerretti DP;	

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XX DR WPI; 1995-106811/14.
XX DR N-PSDB; AAQ85888.
XX PT New isolated DNA encoding hek-L protein or its fusion products -
XX PT useful as assay reagent or for carrying therapeutic and
XX PT diagnostic compounds to leukaemia cells.
XX PS Claim 21; Page 38; 45pp; English.
XX CC The sequence is that of a novel protein designated hek-L, a protein
XX CC that can bind hek (a cell surface receptor tyrosine kinase). Hek-L
XX CC is the first known ligand for hek and can be used to study cellular
XX CC processes regulated by hek (which may be involved in tumorigenesis).
XX CC It is also an immunogen for antibody production, as a reagent for
XX CC detecting hek or hek-L in in vitro assays, to determine binding of
XX CC hek proteins, to purify hek proteins, and to carry diagnostic or
XX CC cytotoxic agents to particular leukaemia cells that express the hek
XX CC antigen. Hek-L also binds the elk tyrosine kinase receptors.
XX CC See also AAR71481.
XX PS Sequence 201 AA;
XX SQ

Query Match 100.0%; Score 1091; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 8.5e-111;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLLPLLRVTLVW-AAFLGSLRGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
Db 1 mrlpllrvtlwaafvlgslrgsslrhvvynssnprllrgdvvvelglndyldivcph 60
QY 61 YEGPGPEGPETFALYMDWPGYESQAEGRPRAYKRWVCSLPTFGHVQFSEKIQRTFPFSL 120
Db 61 yegpgpegpetfalmvdpwgyesqaeqpraykrwvcslpfghvqfsekiqrftpfsl 120
QY 121 GFELPGETYYIVSVPTPESSGCLRLQVSCCKERKSEAHVPVGPESGTSGRGGDT 180
Db 121 gfelfpgetyivsvptpesggclrlqvscckerkksesahvpvpgpesgtsgrwggdt 180
QY 181 PSPICLLLLLLLTLLRLTL 201
Db 181 pspiclllllllllrlrltl 201

RESULT 2
AAR97854
ID AAR97854 standard; Protein; 228 AA.
XX AC AAR97854;
XX DT 05-JAN-1997 (first entry)
XX DE Human AL-1, a ligand for eph-related tyrosine kinase receptor REK7.
XX KW AL-1; REK7; eph-related tyrosine kinase receptor; ligand;
XX KW neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..20
XX FT Modified-site /label= Sig_peptide
XX FT Modified-site /label= Glycosylation
XX FT Modified-site /note="potential N-glycosylation site"
XX FT Binding-site /label= Glycosylation
XX FT Binding-site /note="potential N-glycosylation site"
XX FT Binding-site /label= GPI
XX FT Binding-site /note="potential attachment site for
XX FT glycoposphatidylinositol"

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FT Domain 214...228
FT /label= Hydrophobic_domain
XX WO9613518-A1.
XX PN 09-MAY-1996.
XX PD 26-OCT-1995; 95WO-US14016.
XX PF 07-JUN-1995; 95US-0486449.
XX PR 27-OCT-1994; 94US-0330128.
XX PA (GETH ) GENENTECH INC..
XX PI Caras IW, Winslow JW;
XX XX WPI; 1996-239448/24.
XX DR N-PSDB; AAT18897.
XX PT AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in
XX PT treatment and diagnosis of neuronal disorders and
XX PT angiogenesis-related conditions.
XX PS Claim 1; Page 54; 75pp; English.
XX CC Human AL-1 (AAR97854) neurotrophic factor is a ligand for eph-related
XX CC tyrosine kinase receptor REK7 (AAR97853). Its amino acid sequence
XX CC was deduced from a cDNA clone (AAT18897) isolated from a human foetal
XX CC brain cDNA library. Recombinant, mature AL-1 can be produced in
XX CC transformed host cells. It may be useful in promoting the
XX CC development, maintenance or regeneration of neurons in vivo, and
XX CC can be utilised in methods for the diagnosis and/or treatment of
XX CC neurological disorders. It can also be used to promote or enhance
XX CC angiogenesis. Antagonists and agonists of AL-1, as well as
XX CC antibodies raised against AL-1, also have therapeutic applns.
XX SQ Sequence 228 AA;

Query Match 34.9%; Score 380.5; DB 17; Length 228;
Best Local Similarity 38.3%; Pred. No. 3.5e-33;
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;

QY 1 MRLLPLLRVTLVW-AAFLGSLRGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
Db 4 vemltivflvmcvfsgdpgskavadyavywnssnprfgrdyhidvcindyladvcp 63
QY 60 HYECPGPEGPETFALYMDWPGYESQAEGRPRAYKRWVCSLPTFGHVQFSEKIQRT 116
Db 64 hyedsydpdkterylymvmvndgysacd-htskgkrwecnrphspngplktfsekiqlft 122
QY 117 PPSLGFELPGETYYIVSVPTPESSGQ-CLRLQVSV-----GCK----- 154
Db 123 pflglfepgrgyfysaiaidngrrscldkikvfrptnscmktigvhdvrdvndkve 182
QY 155 ---ERKSEAHVPVGPESGTSGRGGDTPS-PLCLLLLLLLLLILRLRI 200
Db 183 nslpaddvtvhesaep-----srgenaatqprlpsrllaillflamltl 228

RESULT 3
AAW02586
ID AAW02586 standard; Protein; 228 AA.
XX AC AAW02586;
XX DT 28-NOV-1996 (first entry)
XX DE Lerk-7 protein.
XX KW Lerk-6; hek; elk; cell surface receptor; culture; reagent;
XX KW neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
XX KW Lerk-7; probe; cytokine.

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XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..20
XX FT Protein /label= signal_peptide
XX FT Domain 1..228
XX FT Region 1..133 /label= precursor_protein
XX FT Region 134..183 /label= extracellular_receptor-binding_domain
XX FT Region 194..208 /label= spacer_region
XX FT Binding-site 183 /note= "C-terminal stretch of hydrophobic residues"
XX FT 183 /label= GPI_attachment_site
XX PN W09617925-A1.
XX PD 13-JUN-1996.
XX PF 05-DEC-1995; 95WO-US15781.
XX PR 01-MAR-1995; 95US-0396946.
XX PR 06-DEC-1994; 94US-0351025.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Cerretti DP;
XX XX
XX WPI; 1996-287171/29.
XX N-PSDB; AAT32699.
XX
XX New isolated human Lerk-7 cytokine - which binds to cell surface
XX receptors elk, hek and eck, useful for delivering agents to cells or
XX for treating neural disorders
XX
XX Claim 1; Page 37-38; 49pp; English.
XX
XX The present sequence is that of human Lerk-7 protein. Lerk-7 is
XX predicted to be anchored to the cell surface via
XX glycosyl-phosphatidylinositol (GPI) linkage. A GPI anchor attaches to the
XX exposed C-terminal amino acid of the processed mature protein, usually
XX after cleavage upstream, often about 10-12 amino acids, of the N-terminus
XX of the hydrophobic domain. Lerk-7 coding sequence (AAT32699) was isolated
XX using a probe derived from the murine Lerk-6 DNA (AAT32700). The Lerk-7
XX gene and protein can be used for studying the role of Lerk-7 in
XX conjunction with elk, hek and eck receptors. They can also be used for
XX delivering diagnostic or therapeutic agents to cells, e.g. cancer cells.
XX The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic
XX properties and can be used to treat neural tissue disorders.
XX
XX Sequence 228 AA;

Query Match 34.9%; Score 380.5; DB 17; Length 228;
Best Local Similarity 38.3%; Pred. No. 3.5e-33;
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;

QY 1 MRLPLLRVTLVW-AALFGLSPRGSSLRHVYVYVNSNPRLLRGDVAVELGLNDYLDIVCP 59
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 vemltivflvmcvsfqdpgskavadyavyvynssnprfgrgdyhldvcindylvdfcp 63
60 HYESCPGPEGPETFALYVNDWPCYEQACGPRAYKRWCSLPF---GHVQFSEKIQRTT 116
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 hysdvpdkterlyvmvfnfdgsacd-htskgfkrwecnrphspngplkfskqlft 122
117 PFSLGFEFLPGETYYIVISVPTPESSGO-CLRLQVSV-----CCK----- 154
123 pflgfgfrpgrgyfyllsaipdngriscldklkfvrrptnscmkttgvdvndkve 182
QY 155 ---ERKSESAHPYSPGESCTSGWRGGDTPS-PLCLLLLLLLLLLLRLRI 200

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Db 183 nslepaddtvhesaep-----srgenaagtprisrllaillflaml1l 228

RESULT 4
AAW00035
ID AAW00035 standard; Protein; 228 AA.
XX AC AAW00035;
XX DT 24-OCT-1996 (first entry)
XX DE HEK4 binding protein.
XX KW HEK4 binding protein; HEK4 receptor; EPH-like receptor;
XX KW protein tyrosine kinase; ligand; growth; differentiation; cancer;
XX KW nervous system disorder; therapy; antibody.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Protein /label= Sig_peptide
XX FT 20..228
XX FT /label= Mat_protein
XX PN W09623000-A1.
XX PD 01-AUG-1996.
XX PF 16-JAN-1996; 96WO-US01079.
XX PR 27-JAN-1995; 95US-0379802.
XX PA (AMGE-) AMGEN INC.
XX PI Bartley TD, Fox GM;
XX WPI; 1996-362633/36.
XX N-PSDB; AAT34292.
XX
XX Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to
XX modulate growth and differentiation of, e.g. liver and kidney cells,
XX and to treat cancer and nervous system disorders
XX
XX Claim 8; Page 39-40; 65pp; English.
XX
XX Human HEK4 binding protein (HEK4 BP) (AAW00035) binds to and activates
XX HEK4 and ECK receptors. Its amino acid sequence was deduced from
XX a cDNA clone (AAT34292) isolated from a human placenta cDNA library.
XX Expression vectors and host cells can be used for the prodn. of
XX biologically active HEK4 BP. It is useful for modulating the growth
XX and/or differentiation of EPH sub-family receptor-bearing cells,
XX esp. in liver, kidney, lung, skin or neural tissues. It can be
XX used to treat neural system disorders and in the regeneration of
XX damaged or depleted tissues. Antagonists are useful for cancer
XX treatment. HEK4 BP can also be used to raise antibodies.
XX
XX Sequence 228 AA;

Query Match 34.9%; Score 380.5; DB 17; Length 228;
Best Local Similarity 38.3%; Pred. No. 3.5e-33;
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;

QY 1 MRLPLLRVTLVW-AALFGLSPRGSSLRHVYVYVNSNPRLLRGDVAVELGLNDYLDIVCP 59
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 vemltivflvmcvsfqdpgskavadyavyvynssnprfgrgdyhldvcindylvdfcp 63
60 HYESCPGPEGPETFALYVNDWPCYEQACGPRAYKRWCSLPF---GHVQFSEKIQRTT 116
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 hysdvpdkterlyvmvfnfdgsacd-htskgfkrwecnrphspngplkfskqlft 122
QY 117 PFSLGFEFLPGETYYIVISVPTPESSGO-CLRLQVSV-----CCK----- 154

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to also be immunogen for antibody production, as a reagent for







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XX SQ Sequence 204 AA;
Query Match 31.4%; Score 343; DB 22; Length 204;
Best Local Similarity 38.7%; Pred. No. 3.7e-29;
Matches 79; Conservative 26; Mismatches 73; Indels 26; Gaps 5;
QY 11 LWAFLGSLRGGSSLRHVWYNSNPRLLRGDAVVELGLNDYIDVCPHYEGPPEGP 70
DB 4 lwaplglccslaaadrhtvwnsnpkfrnedytihvqndydlciphedhsadaam 63
QY 71 ETALYVMDWPGYSCQAEGPRAYKRWCSLP---FGHVQFSEKIQRFTFSLGFEPLPG 127
DB 64 eqvilyiveheeyqlcpqg-kdqvrcqncrpsakhgpeklsekfqftftlgkefeg 122
QY 128 ETYYIVISVPPESSGQCLRLQVSCCKERKESAHPPVSGPESGTSQWRGDTSPS----- 182
DB 123 hsyvyskphqhdrciriktvtsgkithspqah--dnpgkrla-----addpevrvlh 176
QY 183 -----PLCLLLLLLLLLL 195
DB 177 sighsaaprlfplawtvlilplll 200
RESULT 12
AAR94766
ID AAR94766 standard; Protein; 209 AA.
XX
AC AAR94766;
XX
DT 02-JUL-1996 (first entry)
XX
DE Mouse EPH receptor ligand Elf-1.
XX
KW Elf-1; EPH receptor ligand; dementia; tachycardia; therapy;
KW diagnosis; transgenic animal.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Protein 21..209
FT /label= Mat_protein
FT Region 69..159
FT /label= Cys4_motif
FT Region 35..166
FT /label= Core_sequence_motif
FT Modified-site 38
FT /note= "potential N-glycosylation site"
FT Modified-site 170
FT /note= "potential N-glycosylation site"
FT Modified-site 184
FT /note= "potential N-glycosylation site"
XX
XX WO9609384-A1.
XX
XX 28-MAR-1996.
XX
XX 19-SEP-1995; 95WO-US11869.
XX
XX 27-FEB-1995; 95US-0393462.
XX 19-SEP-1994; 94US-0308814.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Cheng H, Flanagan JG;
XX WPI; 1996-188446/19.
XX DR N-PSDB; AAT15008.
XX
XX Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis
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PT and treatment of disorders associated with the Elf-1 gene, e.g.
PT dementia, tachycardia , etc.
XX
XX Claim 1; Page 86; 107pp; English.
XX
CC A novel mouse EPH receptor ligand, Elf-1 (AAR94766), is involved in
CC the formation and maintenance of ordered spatial arrangements of
CC differentiated tissue. It is the product of a cDNA clone (AAT15008)
CC obtd. from an embryo mid- and hind-brain cDNA expression library.
CC This cDNA is used for the prodn. of recombinant Elf-1, which can
CC be used to modulate proliferation, survival and/or differentiation
CC of cells and tissues, and to stimulate or antagonise intracellular
CC signal transduction pathways mediated by the EPH-type receptor.
XX
SQ Sequence 209 AA;
Query Match 31.4%; Score 342.5; DB 17; Length 209;
Best Local Similarity 42.5%; Pred. No. 4.4e-29;
Matches 90; Conservative 20; Mismatches 67; Indels 35; Gaps 10;
QY 3 LLPLLRVTLWAAFLGSPLRG-----GSSLRHVWYNSNPRLL-----RGDAVVELG 49
DB 8 llpllllll-----plarnedparanadryavvwnsrnprfqsavdggytvevs 60
QY 50 LNDYLDIVCPHYEGPPEP-EGPETFALYVMDWPGYSCQAEGPRAYKRWVC-----SLPFGH 105
DB 61 indyldiycphygaplppaermeryillymvmvgeghascd-hrgrgfkrcwcnrpaapggp 119
QY 106 VQFSEKIQRFTFSLGFEPLGFTYYIISVPTPESSGQ-CLRLQVSV-CCKERKESAHPP 163
DB 120 lkfsekqlftfslgfeftprgheyvysatpnlvdrcplrkivvyrpntleyapep 179
QY 164 VGSPGESGTSQWRGDTSPPLCLLLLLLLLLL 195
DB 180 ift-snsscs9lgg-----chlftttvpvl 203
RESULT 13
AAW71006
ID AAW71006 standard; Protein; 209 AA.
XX
AC AAW71006;
XX
DT 20-OCT-1998 (first entry)
XX
DE Amino acid sequence of a mammalian Elf-1 protein.
XX
KW Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand;
KW B61; LERK-2; proliferation; differentiation; intracellular signalling;
KW increased; survival; neuronal cell; neuron survival; treatment;
KW Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage;
KW bone formation.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FH Peptide 1..20
XX FT /note= "signal peptide"
XX FT Protein 21..209
XX FT /note= "mature protein"
XX FT Modified-site 38
XX FT /note= "potential N-linked glycosylation site"
XX FT Misc-difference 35..166
XX FT /note= "contains core sequence motif"
XX FT Misc-difference 69..159
XX FT /note= "contains a Cys4 motif"
XX FT Modified-site 170
XX FT /note= "potential N-linked glycosylation site"
XX FT Modified-site 184
XX FT /note= "potential N-linked glycosylation site"
XX
XX US5795734-A.
```

XX 18-AUG-1998.  
 XX 31-MAY-1995; 95US-0455001.  
 XX 31-MAY-1995; 95US-0455001.  
 XX 19-SEP-1994; 94US-0308814.  
 XX 27-FEB-1995; 95US-0393462.  
 XX (HARD ) HARVARD COLLEGE.  
 XX Cheng H, Flanagan JG;  
 XX WPI; 1998-466665/40.  
 XX N-PSDB; AAV42926.  
 XX Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor  
 XX - for production of Elf-1 protein, useful for regulating  
 XX proliferation, differentiation, and survival of cells  
 XX Claim 1; Fig 2A; 53pp; English.  
 XX The present sequence represents a mammalian EPH receptor ligand  
 XX designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is  
 XX a tyrosine kinase ligand, which is linked to the membrane through a  
 XX phosphatidylinositol linkage. It shares some homology to 2 other EPH  
 XX receptor ligands, B61 and LERK-2. The Elf-1 protein modulates  
 XX proliferation, differentiation and survival of EPH receptor-expressing  
 XX cells by stimulating or antagonising intracellular signalling mediated  
 XX by the EPH receptor. Typical of many potential applications are  
 XX increasing survival of neuronal cells in culture (e.g. where intended for  
 XX transplantation), also therapeutically in increase neuron survival  
 XX (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent  
 XX nervous system and lymphatic tumours, to induce differentiation of  
 XX hepatocytes to form an artificial liver, to induce cartilage and bone  
 XX formation.  
 XX Sequence 209 AA;  
 SQ  
 Query Match 31.4%; Score 342.5; DB 19; Length 209;  
 Best Local Similarity 42.5%; Pred. No. 4.4e-29;  
 Matches 90; Conservative 20; Mismatches 67; Indels 35; Gaps 10;  
 QY 3 LPLRLTVLWAAFLGSLRG-----GSLRHVVYWNSSNPRLL-----RGDAVVEIG 49  
 Db 8 lpllllll-----plarnedparanadryavynrsprfqvsavdggytvevs 60  
 QY 50 LNDYLDIVCPHYEGPGPP-EGPETALYMDVMPGVESCOAEGPRAYKRWVC---SLPFGH 105  
 Db 61 lndyldiycphygaplpaaermeryilymynvgeghascd-hrqgrkfwecnrpaapggp 119  
 QY 106 VQFSKIQRTFPLSGFFFLPGCTYYIISVTPPESSGO-CLRLOVSV-CCKERKSESAHP 163  
 Db 120 lkfsekqlftfslgfeirpghyeyisatpnlvdrcrlkvyvtrptnetlyeap 179  
 QY 164 VGSPEGSGTSGWRGGDTPSLCLLLLLLLLLL 195  
 Db 180 lft-snsccsglgg-----chflftcpvl 203  
 RESULT 14  
 ID AAY06822  
 XX AAY06822 standard; Protein; 213 AA.  
 XX AC AAY06822;  
 XX 24-JUN-1999 (first entry)  
 XX Human LERK-6 polypeptide.  
 XX LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury;  
 XX cell proliferation; neural growth; neural tissue; neurological disease;  
 KW

KW neurodegenerative; excitotoxicity.  
 XX Homo sapiens.  
 XX WO9910495-A1.  
 XX 04-MAR-1999.  
 XX 27-AUG-1998; 98WO-US17772.  
 XX 29-AUG-1997; 97US-0920440.  
 XX (IMMV ) IMMUNEX CORP.  
 XX Cerretti DP;  
 XX WPI; 1999-243567/20.  
 XX N-PSDB; AAX32767.  
 XX New cytokine designated LERK-6  
 XX Claim 6; Page 42; 46pp; English.  
 XX The invention relates murine and human LERK-6 polypeptides that bind to  
 XX hek/elk receptors. Host cells transfected or transformed with vectors  
 XX comprising the LERK-6 nucleic acid sequences are used for the recombinant  
 XX production of the proteins. LERK-6 polypeptides may be useful in the  
 XX enhancement, stimulation, proliferation or growth of cells expressing the  
 XX hek or elk receptor. The ligand and receptor complex may be involved in  
 XX neural growth, development and/or maintenance. LERK-6 can be used for  
 XX treating disorders of neural tissue such as injury or neurological  
 XX diseases, either chronic or acute. LERK-6 may be employed in treating  
 XX neurodegenerative conditions where there is neural death, excitotoxicity.  
 XX In addition, they may be administered to a mammal to exert a trophic  
 XX effect on neural tissue. They can also be used as reagents for those  
 XX conducting quality assurance studies e.g. to monitor shelf life and  
 XX stability of elk protein under different conditions. The polypeptides can  
 XX also be used as carriers for delivering agents attached to cells bearing  
 XX the elk or hek cell surface receptor. The present sequence represents a  
 XX human LERK-6 polypeptide.  
 XX Sequence 213 AA;  
 SQ  
 Query Match 31.2%; Score 340.5; DB 20; Length 213;  
 Best Local Similarity 41.7%; Pred. No. 7.4e-29;  
 Matches 90; Conservative 21; Mismatches 66; Indels 39; Gaps 10;  
 QY 3 LPLRLTVLWAAFLGSL-----RGSSLRHVYWNSSNPRLLRGDA-----V 45  
 Db 8 lpllllll-----pippbfaraadaaransdryavynrsprfhagagddgggyt 60  
 QY 46 VELGLNDYLDIVCPHYEGPGPP-EGPETALYMDVMPGVESCOAEGPRAYKRWVC---SL 101  
 Db 61 velsandylidycphygaplpaaermehyilymynvgeghascd-hrqgrkfwecnrpaa 119  
 QY 102 PFGHVQFSKIQRTFPLSGFFFLPGCTYYIISVTPPESSGO-CLRLOVSV-CCKERKSE 159  
 Db 120 pggplkfsekqlftfslgfeirpghyeyisatpnavdrpcrlkvyvtrptnetlye 179  
 QY 160 SAHPVGSPEGSGTSGWRGGDTPSLCLLLLLLLLLL 195  
 Db 180 apeiftsnscs--pgg-----crflstipvl 207  
 RESULT 15  
 ID AAB50990  
 XX AAB50990 standard; Protein; 205 AA.  
 XX AC AAB50990;  
 XX 21-MAR-2001 (first entry)  
 XX

Db	4	lwapllglcoslaaarhrtvfwnsnpkfrnedytihvqIndyvdilicphyedhsvadaa	63
Qy	71	-ETFALYMDWPQYESQAGPRAYKRWVCSLP--FGHVQFSEKIQRTFTPSLGFLEPL	126
Db	64	medyilylveheeyqicqps-kdvrwqcnrpsakhgekisekqrfuflgkfkfe	122
Qy	127	GETYYIVSPTPESSQCLRLQVSCCKERKSESAHPVSGESGTSGRWGDTPS----	182
Db	123	ghsyyylskpihqhedrclrlkvtvsgkithspqah--dnpekrila---addpevrvl	176
Qy	183	-----PICLLLLLLLLLIL	195
Db	177	hsichsaaprlfplawtvlilppll	201

```
Query Match          30.8%; Score 335.5; DB 22; Length 205;
Best Local Similarity 38.5%; Pred. No. 2.5e-28;
Matches 79; Conservative 27; Mismatches 72; Indels 27; Gaps 6;

QY      11 LWAATGSPLRGGSSLRHYVYNSSNPRLLRGDAVELGLNDYLDIVCPHYEGGPPEGP 70
       ||| || :|| :||||||| _ : |||||::|:|||||;
```



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 28, 2002, 01:37:42 ; Search time 29.18 Seconds  
(without alignments)  
168.250 Million cell updates/sec

Title: US-09-904-954-4

Perfect score: 1091

Sequence: 1 MRLPLRLTVLWAAFLGSP.....SPCLLLLLLLLLLRLRL 201

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PTCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1091	100.0	201	1	US-08-240-124-4
2	1091	100.0	201	1	US-08-453-943-4
3	1091	100.0	201	2	US-09-057-121-4
4	1091	100.0	201	4	US-09-358-734-4
5	380.5	34.9	228	1	US-08-442-248-4
6	380.5	34.9	228	1	US-08-440-815-4
7	380.5	34.9	228	3	US-08-379-802-2
8	380.5	34.9	228	3	US-09-048-129-2
9	380.5	34.9	228	4	US-08-486-449-4
10	380.5	34.9	228	4	US-08-486-449-4
11	380.5	34.9	228	5	PCT-US95-15781-5
12	368.5	33.8	234	1	US-08-299-567-5
13	364.5	33.4	238	1	US-08-240-124-2
14	364.5	33.4	238	1	US-08-453-943-2
15	364.5	33.4	238	2	US-09-057-121-2
16	364.5	33.4	238	4	US-09-358-734-2
17	359	32.9	200	1	US-08-455-001-4
18	359	32.9	200	5	PCT-US95-11869-4
19	342.5	31.4	209	1	US-08-455-001-2
20	342.5	31.4	209	4	US-08-308-814-2
21	342.5	31.4	209	5	PCT-US95-11869-2
22	340.5	31.2	213	1	US-09-609-324A-10
23	340.5	31.2	213	2	US-08-920-440B-10
24	340.5	31.2	213	4	US-09-173-492-10
25	340.5	31.2	213	4	US-09-173-133-10
26	334.5	30.7	205	1	US-08-321-162-2
27	334.5	30.7	205	1	US-08-448-736-1

28	334.5	30.7	205	1	US-08-441-216-2
29	334.5	30.7	205	1	US-08-452-779-1
30	334.5	30.7	205	1	US-08-299-567-4
31	334.5	30.7	205	2	US-08-445-065-1
32	334.5	30.7	205	2	US-08-445-065-12
33	334.5	30.7	205	3	US-08-959-524-1
34	334.5	30.7	205	3	US-08-959-524-12
35	330.5	30.3	184	1	US-09-609-324A-2
36	330.5	30.3	184	2	US-08-920-440B-2
37	330.5	30.3	184	4	US-09-173-492-2
38	330.5	30.3	184	4	US-09-173-133-2
39	330.5	30.3	184	4	US-09-165-533-2
40	330.5	30.3	184	5	PCT-US95-12779-2
41	330.5	30.3	184	5	PCT-US95-15781-2
42	308	28.2	179	1	US-08-455-001-5
43	308	28.2	179	5	PCT-US95-11869-5
44	261.5	24.0	104	1	US-09-609-324A-8
45	261.5	24.0	104	2	US-08-920-440B-8

#### ALIGNMENTS

RESULT 1  
US-08-240-124-4  
; Sequence 4, Application US/08240124  
; Patent No. 5516658  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240,124  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 201 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-240-124-4







5

GENERAL INFORMATION:  
APPLICANT: Bartley, Timothy D.  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Ligands for EPH-Like Receptor  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/048,129  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/379,802  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-325  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-048-129-2

Query Match 34.9%; Score 380.5; DB 3; Length 228;  
Best Local Similarity 38.3%; Pred. No. 2.8e-35;  
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;  
QY 1 MRLPLRLTVLW-AAFLGSPLRGGSLRHVVYWNSSNPRLLRGDAVVELGLNDYDIVCP 59  
DB 4 VEMLTFLVFLVMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVICINDYLDVFCP 63  
QY 60 HYGEGPPEGPETFEALYMDWPGYSCQAEGRKAYRWYCSLPF---GHVQFSEKIQRT 116  
DB 64 HVEDSVPEKTERVLYVMYVDFGYSACD-HTSKGFKRWECNRPSPNGPLKFSKXQFLT 122  
QY 117 PSLGFEFLPGETYYIYISVTPTESSGQ-CLRLQVSV-----CKK----- 154  
DB 123 PSLGFEFRPGREYFYVYSSAIPDNGRRSCLKLVFVRPTNSCMKTIGVHDRVFDVNDKVE 182  
QY 155 ---ERKSESAHPVSGESGTSWRRGDDTPS-PLCLLLLLLLLLLLRLRI 200  
DB 183 NSLEPADDTVHESAEP-----SRGENAAQTPIPRISRLAILLLFLAMLTL 228

RESULT 9  
US-09-048-079-2  
Sequence 2, Application US/09048079  
Patent No. 6169167  
GENERAL INFORMATION:  
APPLICANT: Bartley, Timothy D.  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Ligands for EPH-Like Receptor  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/048,079  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/379,802  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-325  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-048-079-2

Query Match 34.9%; Score 380.5; DB 4; Length 228;  
Best Local Similarity 38.3%; Pred. No. 2.8e-35;  
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;  
QY 1 MRLPLRLTVLW-AAFLGSPLRGGSLRHVVYWNSSNPRLLRGDAVVELGLNDYDIVCP 59  
DB 4 VEMLTFLVFLVMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVICINDYLDVFCP 63  
QY 60 HYGEGPPEGPETFEALYMDWPGYSCQAEGRKAYRWYCSLPF---GHVQFSEKIQRT 116  
DB 64 HVEDSVPEKTERVLYVMYVDFGYSACD-HTSKGFKRWECNRPSPNGPLKFSKXQFLT 122  
QY 117 PSLGFEFLPGETYYIYISVTPTESSGQ-CLRLQVSV-----CKK----- 154  
DB 123 PSLGFEFRPGREYFYVYSSAIPDNGRRSCLKLVFVRPTNSCMKTIGVHDRVFDVNDKVE 182  
QY 155 ---ERKSESAHPVSGESGTSWRRGDDTPS-PLCLLLLLLLLLLLRLRI 200  
DB 183 NSLEPADDTVHESAEP-----SRGENAAQTPIPRISRLAILLLFLAMLTL 228

RESULT 10  
US-08-486-449-4  
Sequence 4, Application US/08486449  
Patent No. 6280732  
GENERAL INFORMATION:  
APPLICANT: Caras, Ingrid W.  
APPLICANT: Winslow, John W.  
TITLE OF INVENTION: AL-1 Neurotrophic Factor  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,449  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/330128  
FILING DATE: 27-OCT-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0920P1  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-486-449-4

Query Match 34.9%; Score 380.5; DB 4; Length 228;  
Best Local Similarity 38.3%; Pred. No. 2.8e-35;  
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;  
QY 1 MRLPLRLTLVW-AAFLGSLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59  
DB 4 VEMTLVFLVLMCVFSQDPGSKAVADRYAVYWNSSNPRQGRDYHIDVCINDYLDVFCP 63  
QY 60 HYGPGPGPEPTFALYVMDWPGYESQAEGRAYKRWVCSLPF---GHVQFSEKIQRT 116  
DB 64 HYEDSVPEDKTERVLYVMVNFDCYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFOLET 122  
QY 117 PSLGFEFLPGETYYIISVPTPESSGQ-CLRLQVSV-----CCK----- 154  
DB 123 PSLGFEFLPGREYFYIISAIPOGRRSCLKLVFVRPTNSCMKRTIGVHDRVFDVNDKVE 182  
QY 155 ---ERKSESAPHPVSGPESGTSGRWGDTPTS-PLCLLLLLLLLLLLRLRI 200  
DB 183 NSLEPADDTVHSAEP-----SRGENAAQTPIPSRLAILLLFLAMLLTL 228

RESULT 11  
PCT-US95-15781-5  
Sequence 5, Application PC/TUS9515781  
GENERAL INFORMATION:  
APPLICANT: Cerretti, Douglas P.  
TITLE OF INVENTION: Cytokine Designated LerK-7  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15781  
FILING DATE: 05-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/351,025  
FILING DATE: 06-DEC-1994  
CLASSIFICATION:  
APPLICATION NUMBER: US 08/396,946  
FILING DATE: 01-MAR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2829-WO  
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-15781-5

Query Match 34.9%; Score 380.5; DB 5; Length 228;  
Best Local Similarity 38.3%; Pred. No. 2.8e-35;  
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;  
QY 1 MRLPLRLTLVW-AAFLGSLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59  
DB 4 VEMTLVFLVLMCVFSQDPGSKAVADRYAVYWNSSNPRQGRDYHIDVCINDYLDVFCP 63  
QY 60 HYGPGPGPEPTFALYVMDWPGYESQAEGRAYKRWVCSLPF---GHVQFSEKIQRT 116  
DB 64 HYEDSVPEDKTERVLYVMVNFDCYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFOLET 122  
QY 117 PSLGFEFLPGETYYIISVPTPESSGQ-CLRLQVSV-----CCK----- 154  
DB 123 PSLGFEFLPGREYFYIISAIPOGRRSCLKLVFVRPTNSCMKRTIGVHDRVFDVNDKVE 182  
QY 155 ---ERKSESAPHPVSGPESGTSGRWGDTPTS-PLCLLLLLLLLLLLRLRI 200  
DB 183 NSLEPADDTVHSAEP-----SRGENAAQTPIPSRLAILLLFLAMLLTL 228

RESULT 12  
US-08-299-567-5  
Sequence 5, Application US/08299567  
Patent No. 5747033  
GENERAL INFORMATION:  
APPLICANT: Davis, et al.  
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL  
ACTIVITY OF EPH FAMILY LIGANDS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-6707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/299,567  
FILING DATE: 01-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kempler, Gail M.  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 290  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 234 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-299-567-5



Db 8 LLLLLVPLP LLLAOGPGALGNRHAVYWNSSNQHLLRREGYTVQVNVNDYLDIYCPHYN 67  
QY 63 -----GPGPEGPETETALYVMDWPGYEQAGPRAYKRWCS---LPFGHVQFSEK 111  
Db 68 SSGVGPAGPGPGGAEQVLYVMSRNGYRTCNAS--QGFKRWECHRPAPHSPKIFSEK 125  
QY 112 IQRTFPLGFEPLPGETYYIISVPTPESSGQCLRLQVSVCCCKERKSESAPV 164  
Db 126 FQYSAFSLGYEFHAGHEYIISTPTNHLHWKCLRMKVFVCCASTSHSGEKPV 178

RESULT 15  
US-09-057-121-2  
; Sequence 2, Application US/09057121  
; Patent No. 5969110  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,121  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/240,124  
; FILING DATE:  
; APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426  
; FILING DATE: 30-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/109,745  
; FILING DATE: 20-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SEESE, KATHRYN A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2814-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 238 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-057-121-2

Query Match 33.48; Score 364.5; DB 2; Length 238;  
Best Local Similarity 44.5%; Pred. No. 1.9e-33;  
Matches 77; Conservative 16; Mismatches 67; Indels 13; Gaps 3;  
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Db 8 LLLLLVPLP LLLAOGPGALGNRHAVYWNSSNQHLLRREGYTVQVNVNDYLDIYCPHYN 67

QY 63 -----GPGPEGPETETALYVMDWPGYEQAGPRAYKRWCS---LPFGHVQFSEK 111  
Db 68 SSGVGPAGPGPGGAEQVLYVMSRNGYRTCNAS--QGFKRWECHRPAPHSPKIFSEK 125  
QY 112 IQRTFPLGFEPLPGETYYIISVPTPESSGQCLRLQVSVCCCKERKSESAPV 164  
Db 126 FQYSAFSLGYEFHAGHEYIISTPTNHLHWKCLRMKVFVCCASTSHSGEKPV 178  
Search completed: September 28, 2002, 01:37:42  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2002, 01:43:26 ; Search time 251.33 Seconds  
(without alignments)  
281.495 Million cell updates/sec

Title: US-09-904-954-4  
Perfect score: 1091  
Sequence: 1 MRLPLRLTVAFLGSP.....SPCLLLLLLLILRLIL 201

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues  
Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

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2:	/cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3:	/cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4:	/cgn2_6/ptodata/2/paa/US08_COMB.pep.*
5:	/cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6:	/cgn2_6/ptodata/2/paa/US082_COMB.pep.*
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13:	/cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14:	/cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15:	/cgn2_6/ptodata/2/paa/US091_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	1091	100.0	201	1	PCT-US94-09282-4	Sequence 4, Appli
2	1091	100.0	201	5	US-08-161-132-4	Sequence 4, Appli
3	1091	100.0	201	23	US-09-904-954-4	Sequence 4, Appli
4	1073	98.4	201	16	US-09-214-631-8	Sequence 8, Appli
5	1067.5	97.8	200	11	US-08-730-700A-17	Sequence 17, Appli
6	1067.5	97.8	200	20	US-09-621-595-17	Sequence 17, Appli
7	850	77.9	228	21	US-09-760-443-1064	Sequence 1064, Appli

8	675.5	61.9	964	26	US-60-230-435-1232	Sequence 1232, Ap
9	665	61.0	120	26	US-60-185-360-275	Sequence 275, App
10	600	55.0	776	26	US-60-212-656-335	Sequence 335, App
11	542	49.7	96	26	US-60-163-062-1186	Sequence 1186, Ap
12	380.5	34.9	228	7	US-08-330-128-4	Sequence 4, Appli
13	380.5	34.9	228	7	US-08-396-946-5	Sequence 5, Appli
14	380.5	34.9	228	8	US-08-440-567-4	Sequence 4, Appli
15	380.5	34.9	228	8	US-08-442-245A-4	Sequence 4, Appli
16	380.5	34.9	228	8	US-08-442-249-4	Sequence 4, Appli
17	380.5	34.9	228	9	US-08-578-684-4	Sequence 4, Appli
18	380.5	34.9	228	11	US-08-766-239-4	Sequence 4, Appli
19	380.5	34.9	228	12	US-08-832-660-5	Sequence 5, Appli
20	380.5	34.9	228	19	US-09-570-327-2	Sequence 2, Appli
21	380.5	34.9	335	1	PCT-US01-08631-58196	Sequence 58196, A
22	379.5	34.8	228	16	US-09-214-631-9	Sequence 9, Appli
23	368.5	33.8	234	7	US-08-327-423-5	Sequence 5, Appli
24	366.5	33.6	234	6	US-08-229-402-7	Sequence 7, Appli
25	364.5	33.4	238	1	PCT-US94-09282-2	Sequence 2, Appli
26	364.5	33.4	238	5	US-08-109-745-2	Sequence 2, Appli
27	364.5	33.4	238	5	US-08-161-132-2	Sequence 2, Appli
28	364.5	33.4	238	21	US-09-733-756-2	Sequence 2, Appli
29	364.5	33.4	238	23	US-09-904-954-2	Sequence 2, Appli
30	364.5	33.4	238	23	US-09-948-941-315	Sequence 315, App
31	364.5	33.4	238	23	US-09-948-941-360	Sequence 360, App
32	363.5	33.3	238	16	US-09-214-631-7	Sequence 7, Appli
33	359	32.9	200	7	US-08-393-462-4	Sequence 4, Appli
34	359	32.9	200	15	US-09-135-129-4	Sequence 4, Appli
35	351	32.2	233	11	US-08-730-700A-15	Sequence 15, Appli
36	351	32.2	233	20	US-09-621-595-15	Sequence 15, Appli
37	349.5	32.0	227	11	US-08-730-700A-13	Sequence 13, Appli
38	349.5	32.0	227	20	US-09-621-595-13	Sequence 13, Appli
39	349	32.0	237	11	US-08-730-700A-16	Sequence 16, Appli
40	349	32.0	237	20	US-09-621-595-16	Sequence 16, Appli
41	343	31.4	204	23	US-09-927-796-40	Sequence 40, Appli
42	343	31.4	204	24	US-10-001-054-48	Sequence 48, Appli
43	343	31.4	204	24	US-10-028-072-288	Sequence 288, Appli
44	342.5	31.4	209	7	US-08-393-462-2	Sequence 2, Appli
45	342.5	31.4	209	15	US-09-135-129-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
PCT-US94-09282-4  
; Sequence 4, Application PC/TUS9409282  
; GENERAL INFORMATION:  
; APPLICANT: BECKMANN, M. P.  
; APPLICANT: CERRETTI, DOUGLAS P.  
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
; TITLE OF INVENTION: RECEPTOR HEK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/09282  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: US 08/161,132  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/114,426

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; FILING DATE: 30-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/109,745
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SEESE, KATHRYN A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2814-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-09282-4

Query Match 100.0%; Score 1091; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e-101;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPLRLTTLVLAFLGSLPLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
Db 1 MRLPLRLTTLVLAFLGSLPLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
QY 61 YEGPGPEGPETFALYVMDWPGYESCOAEGPRAYKRWVCSLPFGHVQFSEKIQRTFPFSL 120
Db 61 YEGPGPEGPETFALYVMDWPGYESCOAEGPRAYKRWVCSLPFGHVQFSEKIQRTFPFSL 120
QY 121 GFELPGETYYISVPTPESSGQCLRLQVSVCKKERKSESAPHPVGPESGTSQWRGGDT 180
Db 121 GFELPGETYYISVPTPESSGQCLRLQVSVCKKERKSESAPHPVGPESGTSQWRGGDT 180
QY 181 PSLCLLLLLLLLLLRLRL 201
Db 181 PSLCLLLLLLLLLLRLRL 201

RESULT 2
US-08-161-132-4
; Sequence 4, Application us/08161132
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/161,132
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/114,426
; FILING DATE: 30-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/109,745
; FILING DATE: 20-AUG-1993
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: SEESE, KATHRYN A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2814-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-161-132-4

Query Match 100.0%; Score 1091; DB 5; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e-101;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPLRLTTLVLAFLGSLPLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
Db 1 MRLPLRLTTLVLAFLGSLPLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
QY 61 YEGPGPEGPETFALYVMDWPGYESCOAEGPRAYKRWVCSLPFGHVQFSEKIQRTFPFSL 120
Db 61 YEGPGPEGPETFALYVMDWPGYESCOAEGPRAYKRWVCSLPFGHVQFSEKIQRTFPFSL 120
QY 121 GFELPGETYYISVPTPESSGQCLRLQVSVCKKERKSESAPHPVGPESGTSQWRGGDT 180
Db 121 GFELPGETYYISVPTPESSGQCLRLQVSVCKKERKSESAPHPVGPESGTSQWRGGDT 180
QY 181 PSLCLLLLLLLLLLRLRL 201
Db 181 PSLCLLLLLLLLLLRLRL 201

RESULT 3
US-09-904-954-4
; Sequence 4, Application US/09904954
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; CERRETTI, DOUGLAS P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; RECEPTOR HEK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/904,954
; FILING DATE: 12-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,124
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/114,426
; FILING DATE: 30-AUG-1993
; APPLICATION NUMBER: US 08/109,745
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SEESE, KATHRYN A.
; REGISTRATION NUMBER: 32,172
```

```

; REFERENCE/DOCKET NUMBER: 2814-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-904-954-4

Query Match 100.0%; Score 1091; DB 23; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e-101;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPLRLTVLWAAFLGSLRGGSSLRHVYVWNNSSNPRLLRGDAVVVELGLNDYLDIVCPH 60
Db 1 MRLPLRLTVLWAAFLGSLRGGSSLRHVYVWNNSSNPRLLRGDAVVVELGLNDYLDIVCPH 60

QY 61 YEGPGPEGPETFALYVMDWPGYESQAEGRAYKRWVCSLPGHGVQFSEKIQTPTPFSL 120
Db 61 YEGPGPEGPETFALYVMDWPGYESQAEGRAYKRWVCSLPGHGVQFSEKIQTPTPFSL 120

QY 121 GFEFLPGETYYISVPTPESSGQCLRLQVSVCKKRSSESAHPVSGSPGESGTSWGRGGDT 180
Db 121 GFEFLPGETYYISVPTPESSGQCLRLQVSVCKKRSSESAHPVSGSPGESGTSWGRGGDT 180

QY 181 PSPCLLLLLLLLLLRLRL 201
Db 181 PSPCLLLLLLLLLLRLRL 201

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RESULT 4
US-09-214-631-8
; Sequence 8, Application US/09214631
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; FILE REFERENCE: 11757-23USWO
; CURRENT APPLICATION NUMBER: US/09/214,631
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: PCT/CA97/00473
; EARLIER FILING DATE: 1997-07-04
; EARLIER APPLICATION NUMBER: 60/021,272
; EARLIER FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-631-8

Query Match 98.4%; Score 1073; DB 16; Length 201;
Best Local Similarity 98.5%; Pred. No. 7.2e-100;
Matches 198; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRLPLRLTVLWAAFLGSLRGGSSLRHVYVWNNSSNPRLLRGDAVVVELGLNDYLDIVCPH 60
Db 1 MRLPLRLTVLWAAFLGSLRGGSSLRHVYVWNNSSNPRLLRGDAVVVELGLNDYLDIVCPH 60

QY 61 YEGPGPEGPETFALYVMDWPGYESQAEGRAYKRWVCSLPGHGVQFSEKIQTPTPFSL 120
Db 61 YEGPGPEGPETFALYVMDWPGYESQAEGRAYKRWVCSLPGHGVQFSEKIQTPTPFSL 120

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QY 121 GFEFLPGETYYISVPTPESSGQCLRLQVSVCKKRSSESAHPVSGSPGESGTSWGRGGDT 180
Db 121 GFEFLPGETYYISVPTPESSGQCLRLQVSVCKKRSSESAHPVSGSPGESGTSWGRGGDT 180

QY 181 PSPCLLLLLLLLLLRLRL 201
Db 181 PSPCLLLLLLLLLLRLRL 201

RESULT 5
US-08-730-700A-17
; Sequence 17, Application US/08730700A
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; TITLE OF INVENTION: Method of Activating a Novel Ligand
; TITLE OF INVENTION: Regulatory Pathway
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Room 970
; STREET: 600 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1X5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,700A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,518
; FILING DATE: 13-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydk, Linda M.
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 416-586-3235
; TELEFAX: 416-586-3110
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-730-700A-17

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Query Match 97.8%; Score 1067.5; DB 11; Length 200;
Best Local Similarity 99.0%; Pred. No. 2.6e-99;
Matches 199; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MRLPLRLTVLWAAFLGSLRGGSSLRHVYVWNNSSNPRLLRGDAVVVELGLNDYLDIVCPH 60
Db 1 MRLPLRLTVLWAAFLGSLRGGSSLRHVYVWNNSSNPRLLRGDAVVVELGLNDYLDIVCPH 60

QY 61 YEGPGPEGPETFALYVMDWPGYESQAEGRAYKRWVCSLPGHGVQFSEKIQTPTPFSL 120
Db 61 YEGPGPEGPETFALYVMDWPGYESQAEGRAYKRWVCSLPGHGVQFSEKIQTPTPFSL 120

QY 121 GFEFLPGETYYISVPTPESSGQCLRLQVSVCKKRSSESAHPVSGSPGESGTSWGRGGDT 180
Db 121 GFEFLPGETYYISVPTPESSGQCLRLQVSVCKKRSSESAHPVSGSPGESGTSWGRGGDT 180

QY 181 PSPCLLLLLLLLLLRLRL 201

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Db 180 PSLCLLLLLLLLLLILRL 200

RESULT 6

US-09-621-595-17

; Sequence 17, Application US/09621595

; GENERAL INFORMATION:

; APPLICANT: Pawson, Anthony

; Henkemeyer, Mark

; TITLE OF INVENTION: Method of Activating a Novel Ligand

; Regulatory Pathway

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Room 970

; STREET: 600 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5G 1X5

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/621,595

; FILING DATE: 21-Jul-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/730,700

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Kurdydyk, Linda M.

; REGISTRATION NUMBER: 34,971

; REFERENCE/DOCKET NUMBER: 3153-196

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 416-586-3235

; TELEFAX: 416-586-3110

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 200 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-621-595-17

Query Match 97.8%; Score 1067.5; DB 20; Length 200;  
Best Local Similarity 99.0%; Pred. No. 2.6e-99;  
Matches 199; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MRLLPLRLTVLMAAFLGSLRGSSLRHVYWNSSNPRLRGDAVVELGNDYLDIVCPH 60

|||||

Db 1 MRLLPLRLTVLMAAFLGSLRGSSLRHVYWNSSNPRLRGDAVVELGNDYLDIVCPH 60

|||||

QY 61 YEGPGPEGPETALYMDWMPGYEQCAEGPRAYKRWVCSLPFGHVQFSEKIQRTPEFL 120

|||||

Db 61 YEGPGPEGPETALYMDWMPGYEQCAEGPRAYKRWVCSLPFGHVQFSEKI-RFTPEFL 119

|||||

QY 121 GFELPGETYYIISVTPPESSGQCLRLQVSCCKERKSESAPVGPSPGESGTSGWRGGDT 180

|||||

Db 120 GFELPGETYYIISVTPPESSGQCLRLQVSCCKERKSESAPVGPSPGESGTSGWRGGDT 179

|||||

QY 181 PSLCLLLLLLLLLLILRL 201

|||||

Db 180 PSLCLLLLLLLLLLILRL 200

|||||

RESULT 7

US-09-760-443-1064

; Sequence 1064, Application US/09760443

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PJ212

; CURRENT APPLICATION NUMBER: US/09/760,443

; CURRENT FILING DATE: 2001-01-16

; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 2164

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1064

; LENGTH: 228

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (101)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (152)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (159)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-760-443-1064

Query Match 77.9%; Score 850; DB 21; Length 228;

Best Local Similarity 85.8%; Pred. No. 3.2e-77;

Matches 157; Conservative 3; Mismatches 23; Indels 0; Gaps 0;

QY 1 MRLLPLRLTVLMAAFLGSLRGSSLRHVYWNSSNPRLRGDAVVELGNDYLDIVCPH 60

|||||

Db 37 MRLLPLRLTVLMAAFLGSLRGSSLRHVYWNSSNPRLRGDAVVELGNDYLDIVCPH 96

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QY 61 YEGPGPEGPETALYMDWMPGYEQCAEGPRAYKRWVCSLPFGHVQFSEKIQRTPEFL 120

|||||

Db 97 YEGPXPPEGPETALYMDWMPGYEQCAEGPRAYKRWVCSLPFGHVQFSEKIQRFAPFSL 156

|||||

QY 121 GFELPGETYYIISVTPPESSGQCLRLQVSCCKERKSESAPVGPSPGESGTSGWRGGDT 180

|||||

Db 157 GFELPGETYYIISVTPPESSGQCLRLQVSCCKERKSESAPVGPSPGESGTSGWRGGDT 216

|||||

QY 181 PSP 183

|||||

Db 217 PAP 219

|||||

RESULT 8

US-60-230-435-1232

; Sequence 1232, Application US/60230435

; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

; NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; FILE REFERENCE: CLO00768

; TITLE OF INVENTION: USES THEREOF

; CURRENT APPLICATION NUMBER: US/60/230,435

; CURRENT FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 2991

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1232

; LENGTH: 964

; TYPE: PRT

; ORGANISM: HUMAN

US-60-230-435-1232

Query Match 61.9%; Score 675.5; DB 26; Length 964;

Best Local Similarity 77.2%; Pred. No. 8.6e-59;

Matches 132; Conservative 3; Mismatches 21; Indels 15; Gaps 4;

QY 16 LGSPLRGSSLRHVYWNSSNPRLRGDAVVELGNDYLDIVCPHYEGPGPEGPETFEAL 75

|||||

Db 712 LGSPLRGSSLRHVYWNSSNRLLRGDVAVVELGLNDYLDIVCPHYEGPPEGPETPAL 771  
QY 76 YVMDWPGYESCAEGPRAYKRWVCSLPFGHVQFSEKIQRTFSLGFEFLPGCTETYYIISV 135  
Db 772 YVMDWPGYESCAEGPRAYKRWVCSLPFGHVQFSEKIQRTFSLGFEFLPGCTETYYILL 831  
QY 136 PTPSSGQCLRLQVSVCKKERKSAHPVGPSPGSGTSG---WRGDDTPSP 183  
Db 832 -----HGCVRERGLVACDE--CEDRLPGASQREGDQSSQCHWH----PSP 870  
  
RESULT 9  
US-60-185-360-275  
; Sequence 275, Application US/60185360  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE  
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL000287  
; CURRENT APPLICATION NUMBER: US/60/185,360  
; CURRENT FILING DATE: 2000-02-28  
; NUMBER OF SEQ ID NOS: 342  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 275  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-185-360-275  
  
Query Match 61.0%; Score 665; DB 26; Length 120;  
Best Local Similarity 100.0%; Pred. No. 8.1e-59;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 38 RLLRGDAVVELGLNDYLDIVCPHYEGPPEGPETFALYMDWDPGYESCAEGPRAYKRW 97  
Db 1 RLLRGDAVVELGLNDYLDIVCPHYEGPPEGPETFALYMDWDPGYESCAEGPRAYKRW 60  
  
QY 98 VCSLPGHVQFSEKIQRTFSLGFEFLPGCTETYYISVPTPSSGQCLRLQVSVCKKER 156  
Db 61 VCSLPGHVQFSEKIQRTFSLGFEFLPGCTETYYISVPTPSSGQCLRLQVSVCKKER 119  
  
RESULT 10  
US-60-212-656-335  
; Sequence 335, Application US/60212656  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL000673  
; CURRENT APPLICATION NUMBER: US/60/212,656  
; CURRENT FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 795  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 335  
; LENGTH: 776  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-212-656-335  
  
Query Match 55.0%; Score 600; DB 26; Length 776;  
Best Local Similarity 84.3%; Pred. No. 2.9e-51;  
Matches 107; Conservative 4; Mismatches 16; Indels 0; Gaps 0;  
  
QY 38 RLLRGDAVVELGLNDYLDIVCPHYEGPPEGPETFALYMDWDPGYESCAEGPRAYKRW 97  
Db 590 KLLRGDAVVELGLNDYLDIVCPHYEGPPEGPETFALYMDWDPGYESCAEGPRAYKRW 649  
  
QY 98 VCSLPGHVQFSEKIQRTFSLGFEFLPGCTETYYISVPTPSSGQCLRLQVSVCKKER 157

Db 650 VCSLPGHVQFSEKIQRTFSLGFEFLPGCTETYYISTPHNLHWKCLRMKVFCVCCASTS 709  
QY 158 SESAHPV 164  
Db 710 HSGERPVP 716  
  
RESULT 11  
US-60-163-062-1186  
; Sequence 1186, Application US/60163062  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL000134  
; CURRENT APPLICATION NUMBER: US/60/163,062  
; CURRENT FILING DATE: 1999-11-02  
; NUMBER OF SEQ ID NOS: 1302  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1186  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Human  
US-60-163-062-1186  
  
Query Match 49.7%; Score 542; DB 26; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.8e-46;  
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 38 RLLRGDAVVELGLNDYLDIVCPHYEGPPEGPETFALYMDWDPGYESCAEGPRAYKRW 97  
Db 1 RLLRGDAVVELGLNDYLDIVCPHYEGPPEGPETFALYMDWDPGYESCAEGPRAYKRW 60  
  
QY 98 VCSLPGHVQFSEKIQRTFSLGFEFLPGCTETYYI 133  
Db 61 VCSLPGHVQFSEKIQRTFSLGFEFLPGCTETYYI 96  
  
RESULT 12  
US-08-330-128-4  
; Sequence 4, Application US/08330128  
; GENERAL INFORMATION:  
; APPLICANT: Caras, Ingrid W.  
; APPLICANT: Winslow, John W.  
; TITLE OF INVENTION: AL-1 Neurotrophic Factor  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,128  
; FILING DATE: 27-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Johnston, Sean A.  
; REGISTRATION NUMBER: 35,910  
; REFERENCE/DOCKET NUMBER: 920  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-3562  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-330-128-4

Query Match 34.9%; Score 380.5; DB 7; Length 228;  
Best Local Similarity 38.3%; Pred. No. 1.1e-29;  
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;  
QY 1 MRLPLRLRTVLW-AAFLGSLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59  
Db 4 VEMLTFLVFLVMCMVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63  
QY 60 HYEGPGPEGPETFALYMDVMPGYESQAGPRAYKRWGSLPF---GHVQFSEKIQRT 116  
Db 64 HYEDSVPEDKTERVLYVMVFDGYSACD-HTSKGFKRWCNRPSPNGPLKFKSEKQLFT 122  
QY 117 PFLSGFELPGETYYISVTPPESSGO-CLRLQVSV-----CK----- 154  
Db 123 PFLSGFELPGETYYISVTPPESSGO-CLRLQVSV-----CK----- 154  
QY 155 ---ERKSESAHPVGPESGTSGRGDDTPS-PLCLLLLLLLLLLRLRLRI 200  
Db 183 NSLEPADDTVHESAE-----SRGENAAQTPIPSRLLAILLFLAMLLTL 228

RESULT 13  
US-08-396-946-5  
; Sequence 5, Application US/08396946  
; GENERAL INFORMATION:  
; APPLICANT: Ceretti, Douglas P.  
; TITLE OF INVENTION: Cytokine Designated Lerk-7  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/396,946  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/351,025  
; FILING DATE: 06-DEC-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2829-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-396-946-5

Query Match 34.9%; Score 380.5; DB 7; Length 228;  
Best Local Similarity 38.3%; Pred. No. 1.1e-29;  
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;  
QY 1 MRLPLRLRTVLW-AAFLGSLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59  
Db 4 VEMLTFLVFLVMCMVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63  
QY 60 HYEGPGPEGPETFALYMDVMPGYESQAGPRAYKRWGSLPF---GHVQFSEKIQRT 116  
Db 64 HYEDSVPEDKTERVLYVMVFDGYSACD-HTSKGFKRWCNRPSPNGPLKFKSEKQLFT 122  
QY 117 PFLSGFELPGETYYISVTPPESSGO-CLRLQVSV-----CK----- 154  
Db 123 PFLSGFELPGETYYISVTPPESSGO-CLRLQVSV-----CK----- 154  
QY 155 ---ERKSESAHPVGPESGTSGRGDDTPS-PLCLLLLLLLLLLRLRLRI 200  
Db 183 NSLEPADDTVHESAE-----SRGENAAQTPIPSRLLAILLFLAMLLTL 228

RESULT 14  
US-08-440-567-4  
; Sequence 4, Application US/08440567  
; GENERAL INFORMATION:  
; APPLICANT: Caras, Ingrid W.  
; APPLICANT: Winslow, John W.  
; TITLE OF INVENTION: AL-1 Neurotrophic Factor  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,567  
; FILING DATE: 15-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/330128  
; FILING DATE: 27-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: 920C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-8674  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-440-567-4

Query Match 34.9%; Score 380.5; DB 8; Length 228;  
Best Local Similarity 38.3%; Pred. No. 1.1e-29;  
Matches 88; Conservative 32; Mismatches 75; Indels 35; Gaps 8;  
QY 1 MRLPLRLRTVLW-AAFLGSLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59  
Db 4 VEMLTFLVFLVMCMVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

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Qy 155 ---ERKSESANHPVSGPESGTSWGRGGTPS--PLCLLLLLLLLLLLLRLRI 200
Db 183 NSLEPADDTVHESAEP---SRGENAAQTTPRPSRLAILLFLAAMLLTL 228

Search completed: September 28, 2002, 01:43:27
Job time: 892 sec

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Search completed: September 28, 2002, 01:43:27  
Job time: 892 sec

		Query Match	34.9%	Score 380.5;	DB 8;	Length 228;
		Best Local Similarity	38.3%;	Pred. No. 1.1e-29;		
		Matches 88; Conservative	32;	Mismatches 75;	Indels 35;	Gaps 8;
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Qy	1	MRLPLLRTVLW-AAFLGSLPLGGSSLRHYVYWNSSNPRLLRGDAVVELGLNDYLDI	VCP	59		
	:	: :   :		:	: :	
Dd	4	VEMLTLFVLWMCVFGSDPGSKAVADRYAYVNSSNPFRFGDYHIDVCINDYLDVFEC		63		
	:	: :   :		:	: :	
Qy	60	HYEGPPEGPETPALYNMVDMPYESCOAEGPRAYKRWC	SLPF---	GHVGFSEKIQRT	116	
	:	: :   :		:	: :	
Dd	64	HYESVPEDKTERVLYMNVEDGYACD-HTSKGFKRWECNRPHSPNGPLAFSEKFQLFT		122		
	:	: :   :		:	: :	
Qy	117	PFSLGFEFLPCGETYYTISVTPESPSSGO-CCLRQYSV-----CCK-----		154		
	:	: :   :		:	: :	
Dd	123	PFSLGFEFPGRREYFTSALPDGNRGSCLKLKYFVRPTNSCMKTIGVHDHFVDNVDRKE		182		
	:	: :   :		:	: :	





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 28, 2002, 01:45:54 ; Search time 125.93 Seconds  
(without alignments)  
431.292 Million cell updates/sec

Title:.. US-09-904-954-4

Perfect score: 1091

Sequence: 1 MRLPLLRVWAAFLGSP.....SPLCLLLLLLLILRLRL 201

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 962758 seqs, 270212090 residues

Total number of hits satisfying chosen parameters: 962758

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*

7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1073	98.4	201	6	US-10-138-787-8
2	850	77.9	228	6	US-10-206-021-615
3	850	77.9	228	6	US-10-212-054-1064
4	379.5	34.8	228	6	US-10-138-787-9
5	363.5	33.3	233	6	US-10-138-787-7
6	343	31.4	204	1	PCT-US02-24563-288
7	343	31.4	204	6	US-10-121-049-288
8	343	31.4	204	6	US-10-121-050-288
9	343	31.4	204	6	US-10-121-053-288
10	343	31.4	204	6	US-10-121-043-288
11	343	31.4	204	6	US-10-121-044-288
12	343	31.4	204	6	US-10-121-047-288
13	343	31.4	204	6	US-10-121-054-288
14	343	31.4	204	6	US-10-121-056-288
15	343	31.4	204	6	US-10-121-057-288
16	343	31.4	204	6	US-10-121-058-288
17	343	31.4	204	6	US-10-121-060-288
18	343	31.4	204	6	US-10-121-063-288
19	343	31.4	204	6	US-10-123-108-288
20	343	31.4	204	6	US-10-123-154-288
21	343	31.4	204	6	US-10-123-156-288
22	343	31.4	204	6	US-10-123-157-288
23	343	31.4	204	6	US-10-123-212-288
24	343	31.4	204	6	US-10-123-213-288
25	343	31.4	204	6	US-10-123-109-288
26	343	31.4	204	6	US-10-121-041-288

27	343	31.4	204	6	US-10-121-045-288	Sequence 288, App
28	343	31.4	204	6	US-10-121-046-288	Sequence 288, App
29	343	31.4	204	6	US-10-121-051-288	Sequence 288, App
30	343	31.4	204	6	US-10-121-040-288	Sequence 288, App
31	343	31.4	204	6	US-10-121-048-288	Sequence 288, App
32	343	31.4	204	6	US-10-121-052-288	Sequence 288, App
33	343	31.4	204	6	US-10-121-061-288	Sequence 288, App
34	343	31.4	204	6	US-10-121-042-288	Sequence 288, App
35	343	31.4	204	6	US-10-121-055-288	Sequence 288, App
36	343	31.4	204	6	US-10-121-059-288	Sequence 288, App
37	343	31.4	204	6	US-10-124-822-288	Sequence 288, App
38	343	31.4	204	6	US-10-123-903-288	Sequence 288, App
39	343	31.4	204	6	US-10-124-817-288	Sequence 288, App
40	343	31.4	204	6	US-10-124-819-288	Sequence 288, App
41	343	31.4	204	6	US-10-124-823-288	Sequence 288, App
42	343	31.4	204	6	US-10-125-704-288	Sequence 288, App
43	343	31.4	204	6	US-10-123-215-288	Sequence 288, App
44	343	31.4	204	6	US-10-123-235-288	Sequence 288, App
45	343	31.4	204	6	US-10-123-236-288	Sequence 288, App

#### ALIGNMENTS

RESULT 1

US-10-138-787-8

; Sequence 8, Application US/10138787

; GENERAL INFORMATION: Sacha

; APPLICANT: Mbamalu, Geraldine

; APPLICANT: Pawson, Tony

; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

; TITLE OF INVENTION: TYROSINE KINASES

; FILE REFERENCE: 11757.23USWO

; CURRENT APPLICATION NUMBER: US/10/138.787

; PRIOR FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US/09/214,631

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: PCT/CA97/00473

; PRIOR FILING DATE: 1997-07-04

; PRIOR APPLICATION NUMBER: 60/021,272

; PRIOR FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 201

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-138-787-8

Query Match 98.4%; Score 1073; DB 6; Length 201;  
Best Local Similarity 98.5%; Pred. No. 2.4e-97;  
Matches 198; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRLPLLRVWAAFLGSPGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Db 1 MRLPLLRVWAAFLGSPGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Qy 61 YEGPGPPGPEPTFALYMDWPGYEQAGPRAYKRWKVCSLPFGHVQFSEKIQRTTFPSL 120

Db 61 YEGPGPPGPEPTFALYMDWPGYEQAGPRAYKRWKVCSLPFGHVQFSEKIQRTTFPSL 120

Qy 121 GFEPFLPGETYYIISVPTPESSQCLRLQVSCCKKESAHVPVSGPSGSGTSGWRGDT 180

Db 121 GFEPFLPGETYYIISVPTPESSQCLRLQVSCCKKESAHVPVSGPSGSGTSGWRGDT 180

Qy 181 PSLCLLLLLLLLLLLRLRL 201

Db 181 PSLCLLLLLLLLLLLRLRL 201



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Db 123 PFLGFEPPGKREYFYISAIKPNRRSCLKLKVEFRNTSCMKITGVHDRVFDVNDKVE 182
Qy 155 --ERKSESAPVSGSGTSGWRGGDTPS-PLCLLLLLLLLLLRLRLRI 200
Db 183 NSLEPADTTHESAEP-----SRGENAACTPRIPSRLLAILLFLAMLLTL 228

RESULT 5
US-10-138-787-7
; Sequence 7, Application US/10138787
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mmamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/10/138,787
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/214,631
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/CA97/00473
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: 60/021,272
; PRIOR FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-7

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Query Match 33.3%; Score 363.5; DB 6; Length 233;
Best Local Similarity 46.2%; Pred. No. 1.6e-27;
Matches 78; Conservative 16; Mismatches 56; Indels 19; Gaps 6;

Qy 3 LPLRLTLWAAFLGSLRGGSSLRHVYVWNSNPRLLRGDAVVELGNDYLDIVCPHYE 62
Db 17 LPLRL-----AGP-AGALGNRHAVYVWNSNHLRREGTYVQVNDYLDIVCPHYN 67

Qy 63 -----GPGPEGPETALYMDVPGYSCQAGPRAYKRWVCS- --LPFGHVQFSEKIQRF 115
Db 68 SSGAGPGPGGGAE--IVLYMSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKSEKFOR 124

Qy 116 TFLSLGFELPGETYYISVPTPESSGQCLRLQVSVCCCKERKSESAPHV 164
Db 125 SAFSLGYEFHAGHEYIYSTPTPHNLHWKCLRMKVFVCCASTSHSGKPV 173

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RESULT 6
PCT-US02-24563-288
; Sequence 288, Application PC/TUS0224563
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

```

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: PCT/US02/24563
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
PCT-US02-24563-288

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Query Match 31.4%; Score 343; DB 1; Length 204;
Best Local Similarity 38.7%; Pred. No. 1.4e-25;
Matches 79; Conservative 26; Mismatches 73; Indels 26; Gaps 5;

Qy 11 LWAAFLGSLRGGSSLRHVYVWNSNPRLLRGDAVVELGNDYLDIVCPHYEGPPEGP 70
Db 4 LWAPLLGLCCSLAAADRTHTVFNWNSNPKERNEDYTHVQLNDYVLIICPHYEDHSDAAM 63

Qy 71 ETTFALYMDVPGYSCQAGPRAYKRWVCSLP---FGHVQFSEKIQRFPPFSLGFEFLPG 127
Db 64 EQYILVLYHEHEYQLCPQS-KDQVRWQCNRPSSAKHGPEKLSKFORFTPTLKGFEKREG 122

Qy 128 ETYVYISVPTPESSGQCLRLQVSVCCCKERKSESAPVSGESCTSGWRGGDTPS----- 182
Db 123 HSYVYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPVVRVLH 176

Qy 183 -----PLCLLLLLLLLLL 195
Db 177 SIGHSAPRLPFLPANTVLLPLLL 200

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RESULT 7
US-10-121-049-288
; Sequence 288, Application US/10121049
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

```

; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330RIC17  
; CURRENT APPLICATION NUMBER: US/10/121,049  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 288  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-121-049-288

Query Match 31.4%; Score 343; DB 6; Length 204;  
Best Local Similarity 38.7%; Pred. No. 1.4e-25;  
Matches 79; Conservative 26; Mismatches 73; Indels 26; Gaps 5;

QY 11 LWAFLGSLRGSSLRHVYVWNSNPRLLRGDVAVVELGLNDYLDIVCPHYEGPGPEGP 70  
Db 4 LWAPLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTHVQLNDYVDIICPHYEDHSDAAM 63  
QY 71 ETFALYVMDPVGESQAEGRAYKRWGCSLP---FGHVQFSEKIQRTFPPFSLGFEFLPG 127  
Db 64 EQVILYVHEEYQLCQPOS-KDQVRWQCNRPFSAKHGPEKLSKFORFTFTFLGKFEKEG 122  
QY 128 ETYYISVTPPESSGQCLRLQVSVCKKESAHVPVSGSGTSGWRGGDTPS-----182  
Db 123 HSYIYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPVRLVH 176  
QY 183 -----PLCLLLLLLLLLL 195  
Db 177 SIGHSAAPRLFLPLAWTVLLPLLL 200

RESULT 8  
US-10-121-050-288  
; Sequence 288, Application US/10121050  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330RIC20  
; CURRENT APPLICATION NUMBER: US/10/121,050  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 288  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-121-050-288

Query Match 31.4%; Score 343; DB 6; Length 204;  
Best Local Similarity 38.7%; Pred. No. 1.4e-25;  
Matches 79; Conservative 26; Mismatches 73; Indels 26; Gaps 5;  
QY 11 LWAFLGSLRGSSLRHVYVWNSNPRLLRGDVAVVELGLNDYLDIVCPHYEGPGPEGP 70  
Db 4 LWAPLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTHVQLNDYVDIICPHYEDHSDAAM 63  
QY 71 ETFALYVMDPVGESQAEGRAYKRWGCSLP---FGHVQFSEKIQRTFPPFSLGFEFLPG 127  
Db 64 EQVILYVHEEYQLCQPOS-KDQVRWQCNRPFSAKHGPEKLSKFORFTFTFLGKFEKEG 122

QY 128 ETYYISVTPPESSGQCLRLQVSVCKKESAHVPVSGSGTSGWRGGDTPS-----182  
Db 123 HSYIYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPVRLVH 176  
QY 183 -----PLCLLLLLLLLLL 195  
Db 177 SIGHSAAPRLFLPLAWTVLLPLLL 200

RESULT 9  
US-10-121-053-288  
; Sequence 288, Application US/10121053  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330RIC23  
; CURRENT APPLICATION NUMBER: US/10/121,053  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 288  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-121-053-288

Query Match 31.4%; Score 343; DB 6; Length 204;  
Best Local Similarity 38.7%; Pred. No. 1.4e-25;  
Matches 79; Conservative 26; Mismatches 73; Indels 26; Gaps 5;  
QY 11 LWAFLGSLRGSSLRHVYVWNSNPRLLRGDVAVVELGLNDYLDIVCPHYEGPGPEGP 70  
Db 4 LWAPLLGLCCSLAAADRHTVFNWSSNPKFRNEDYTHVQLNDYVDIICPHYEDHSDAAM 63  
QY 71 ETFALYVMDPVGESQAEGRAYKRWGCSLP---FGHVQFSEKIQRTFPPFSLGFEFLPG 127  
Db 64 EQVILYVHEEYQLCQPOS-KDQVRWQCNRPFSAKHGPEKLSKFORFTFTFLGKFEKEG 122  
QY 128 ETYYISVTPPESSGQCLRLQVSVCKKESAHVPVSGSGTSGWRGGDTPS-----182  
Db 123 HSYIYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPVRLVH 176  
QY 183 -----PLCLLLLLLLLLL 195

[illegible]

```
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-047-288

Query Match          31.4%; Score 343; DB 6; Length 204;
Best Local Similarity 38.7%; Pred. No. 1.4e-25;
Matches 79; Conservative 26; Mismatches 73; Indels 26; Gaps 5;

QY 11 LWAFLGSLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPPEGP 70
    ||| || : : ||| ||| : : : ||| ||| |||
Db 4 LWAPLGLCCSLAAADRHVFNWSSNPKFRNEDYTHVQLNDYVDICPHYEDHSADAAM 63
    ||| || : : ||| ||| : : : ||| ||| |||
QY 71 ETFALYMDVMPGYESCOAGPRAYKRWVCSLP---FGHVQFSEKIQRTFPSLGFELPG 127
    | : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 EQYILVLEHEEYQLCQPOS-KQVWRQCNRPSAKHGPEKLFSEKFORFTFTLGKEFEG 122
    | : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 128 ETTYIISVPTPESSGQCLRLQVSCCKERKESAHVPVGPESGTSWGRGGDTPS----- 182
    : ||| || : : ||| ||| : | : ||| ||| : | : ||| ||| : | : ||| |||
Db 123 HSYIYISKPIHQHEDRCLRLKVTVSGKITHSPOAH--DNPQEKRLA-----ADPEVRVLH 176
    : ||| || : : ||| ||| : | : ||| ||| : | : ||| ||| : | : ||| |||
QY 183 -----PLCLLLLLLLLLL 195
    || : ||| |||
Db 177 SIGHSAAPRLFLPLAWTVLLPLLL 200
    || : ||| |||

RESULT 14
US-10-121-056-288
; Sequence 288, Application US/10121056
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC25
; CURRENT APPLICATION NUMBER: US/10/121,056
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-056-288

Query Match          31.4%; Score 343; DB 6; Length 204;
Best Local Similarity 38.7%; Pred. No. 1.4e-25;
Matches 79; Conservative 26; Mismatches 73; Indels 26; Gaps 5;

QY 11 LWAFLGSLRGSSLRHVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPPEGP 70
    ||| || : : ||| ||| : : : ||| ||| |||
Db 4 LWAPLGLCCSLAAADRHVFNWSSNPKFRNEDYTHVQLNDYVDICPHYEDHSADAAM 63
    ||| || : : ||| ||| : : : ||| ||| |||
QY 71 ETFALYMDVMPGYESCOAGPRAYKRWVCSLP---FGHVQFSEKIQRTFPSLGFELPG 127
    | : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 EQYILVLEHEEYQLCQPOS-KQVWRQCNRPSAKHGPEKLFSEKFORFTFTLGKEFEG 122
    | : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 128 ETTYIISVPTPESSGQCLRLQVSCCKERKESAHVPVGPESGTSWGRGGDTPS----- 182
    : ||| || : : ||| ||| : | : ||| ||| : | : ||| ||| : | : ||| |||
Db 123 HSYIYISKPIHQHEDRCLRLKVTVSGKITHSPOAH--DNPQEKRLA-----ADPEVRVLH 176
    : ||| || : : ||| ||| : | : ||| ||| : | : ||| ||| : | : ||| |||
QY 183 -----PLCLLLLLLLLLL 195
    || : ||| |||
Db 177 SIGHSAAPRLFLPLAWTVLLPLLL 200
    || : ||| |||

RESULT 15
US-10-121-057-288
; Sequence 288, Application US/10121057
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
```

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C13
; CURRENT APPLICATION NUMBER: US/10/121,057
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-057-288

Query Match 31.4%; Score 343; DB 6; Length 204;  
Best Local Similarity 38.7%; Pred. No. 1.4e-25;  
Matches 79; Conservative 26; Mismatches 73; Indels 26; Gaps 5;

QY	11	LWAAFLGSLRGSSLRHVYVWYVWSSNPRLRLRGDVAVVELGLNDYLDIVCPHYEGPGPEGP	70
DB	4	LWAPLLGLCCSLAARDHTVFNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM	63
QY	71	ETFALYVWDPGYESCQAEGRAYRWVCSLP---FGHVQSEKIQRTFPFSLGFELPG	127
DB	64	EQYILYVHEEYQLCQPOS-KDOVRWQCNRPSAKHGPEKLSKPFQRTFTLGKEFKEG	122
QY	128	ETVYIVSVTPSSGQCLRLQVSCCKERKESAHVPVSGSGTSGWRGGDTPS----	182
DB	123	HSYVYISKFIHQHEDCKLRKVTVSGKITHSPQAH--DNPQEKRLA----ADDPVYRLH	176
QY	183	-----PCLLLLLLLLLL	195
DB	177	SIGHSAAPRLFPPLAWTVLLPLLL	200

Search completed: September 28, 2002, 01:45:54  
Job time: 619 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2002, 01:38:54 ; Search time 49.23 Seconds  
(without alignments)  
392.321 Million cell updates/sec

Title: US-09-904-954-4  
Perfect score: 1091  
Sequence: 1 MRLLPLRLTVLWAAFLGSP.....SPICLLLLLLLLLRLRL 201

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1091	100.0	201	2 I38850	LERK-4 - human
2	380.5	34.9	228	2 I58170	LERK-7 precursor - repulsive axon gui
3	373	34.2	228	2 A57084	LERK-3 - human
4	364.5	33.4	238	2 I38849	ephrin-A2 - human
5	346.5	31.8	213	2 J50322	ELF-1 protein prec
6	342.5	31.4	209	2 A34984	B61 protein transmem
7	334.5	30.7	205	2 A36377	hepatoma transmem
8	164.5	15.1	336	2 I49766	hepatoma transmem
9	156	14.3	333	2 I84743	hepatoma transmem
10	146	13.4	346	2 S46993	elk ligand - human
11	145	13.3	345	2 I58406	LERK-2 - rat
12	144	13.2	345	2 I48780	Stral/Epig2 protei
13	132.5	12.1	462	2 T32645	hypothetical prote
14	113	10.4	237	2 T19914	hypothetical prote
15	87	8.0	628	2 I38000	Lutheran blood gro
16	85	7.8	164	2 F87296	hypothetical prote
17	85	7.8	268	2 S24377	hypothetical prote
18	84	7.7	325	2 I65354	stem cell antigen
19	84	7.7	382	2 I52565	stem cell antigen
20	83.5	7.7	577	1 VGBEGI	glycoprotein E - s
21	83	7.6	198	2 G42148	GTP-binding protei
22	82	7.5	206	2 A84664	probable phytocyan
23	80.5	7.4	564	2 I53106	gene gli protein - rod outer segment
24	80	7.3	351	2 I54347	rod outer segment
25	80	7.3	351	2 I68620	cellulose synthase
26	80	7.3	472	2 AG3600	cellulose synthase
27	79	7.2	278	2 C84266	hypothetical prote
28	78	7.1	620	2 T30765	hypothetical prote
29	77.5	7.1	248	2 H70027	carboxylesterase h

30	77.5	7.1	261	2 B64783	hypothetical prote
31	77.5	7.1	294	2 T22639	hypothetical prote
32	77.5	7.1	310	2 T22641	hypothetical prote
33	77.5	7.1	1616	2 I37183	gene APXL protein
34	77	7.1	582	2 S10099	transcription fact
35	77	7.1	623	2 I46382	ZPI precursor - mo
36	77	7.1	654	2 A34734	transcription fact
37	77	7.1	742	4 C34734	transcription fact
38	77	7.1	825	4 B34734	transcription fact
39	76.5	7.0	200	2 H84715	probable phytocyan
40	76	7.0	502	2 T01378	nicotinic receptor
41	75.5	6.9	219	2 A45384	GTP-binding protei
42	75.5	6.9	685	2 JC7570	Delta-4 protein -
43	75.5	6.9	1503	2 T43166	alpha-2-macroglobu
44	75.5	6.9	2115	2 S38480	nonstructural prot
45	75.5	6.9	6805	2 S20901	titin - rabbit (fr

ALIGNMENTS

RESULT 1  
I38850  
LERK-4 - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 29-Sep-1999  
C:Accession: I38850  
R:Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.  
Oncogene 10, 299-306, 1995  
A:Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs en  
A:Reference number: I38849; MUID:95140419  
A:Accession: I38850  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-201 <RES>  
A:Cross-references: EMBL:U14188; NID:9642834; PIDN:AAC50079.1; PID:9642835  
C:Genetics:  
A:Gene: GDB:EPLG4  
A:Cross-references: GDB:438337; OMIM:601380  
A:Map position: lq21-lq22  
C:Superfamily: axon guidance signal protein

Query Match 100.0%; Score 1091; DB 2; Length 201;  
Best Local Similarity 100.0%; Pred. No. 1.1e-95;  
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLLPLRLTVLWAAFLGSPLRGSSLRHVYVWNSNPRLLRGDVAVVGLGNDYLDIVCPH 60  
Db 1 MRLLPLRLTVLWAAFLGSPLRGSSLRHVYVWNSNPRLLRGDVAVVGLGNDYLDIVCPH 60  
Qy 61 YEGPQPPGPEPFALYVMDVDPGYESCOAGRPAYKRWVCSLPFGHVQFSEKIQRTPTPFSL 120  
Db 61 YEGPQPPGPEPFALYVMDVDPGYESCOAGRPAYKRWVCSLPFGHVQFSEKIQRTPTPFSL 120  
Qy 121 GFEFLPGETYYIISVPTPESSQCLRLQVSCCKERKSESAPVSGSPGSGTSGWRGGDT 180  
Db 121 GFEFLPGETYYIISVPTPESSQCLRLQVSCCKERKSESAPVSGSPGSGTSGWRGGDT 180  
Qy 181 PSPICLLLLLLLLLLLRLRL 201  
Db 181 PSPICLLLLLLLLLLLRLRL 201

RESULT 2  
I58170  
LERK-7 precursor - human  
N:Alternate names: AL-1  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 29-Sep-1999  
C:Accession: I58170; G01812  
R:Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.  
Neuron 14, 973-981, 1995

[illegible]

Db 8 LPLPLLLLLL-----PLPPPPFAPPEDRRRANSRDYAYVWNSRPHAGAGDDGGYTT 60  
 Qy 46 VELGLNDYLDVCPHYEGGPP-EGPETFALYVMDWPGYESQAGPRAYKRWC---SL 101  
 Db 61 VEVSLNDYLDVCPHYGAPLPAERMEHYLYWNGEGHSCD-HRQGRFRWECNRPA 119  
 Qy 102 PFGHVQFSEKIQRTFPFSLGFEFLPGETYYIYISVPTPESSGQ-CLRLQVSV-CCKERKSE 159  
 Db 120 PGGPLKSEKFLQFTFPFSLGFEFRPGHEYYIYISATPPNNAVDPRCLRLKVVYRPTNETIYE 179  
 Qy 160 SHNPVSGSGESTSWRGDTPSPCLLLLLLLLLL 195  
 Db 180 APEPFTSNSSCS--PGG-----CRLFLSTPVL 207

RESULT 6  
 A54984  
 N:ELF-1 protein precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 29-Sep-1999  
 C:Accession: A54984; A55873  
 R:Cheng, H.J.; Flanagan, J.G.  
 Cell 79, 157-168, 1994  
 A:Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the  
 A:Reference number: A54984; MUID:9500776  
 A:Accession: A54984  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-209 <HE>  
 A:Cross-references: GB:U14941; NID:g558836; PIDN:AAA53636.1; PID:g558837  
 R:Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.  
 J. Biol. Chem. 270, 3467-3470, 1995  
 A:Title: cDNA cloning and characterization of a Cdk7 receptor protein-tyrosine kinase 11  
 A:Reference number: A55873; MUID:95181289  
 A:Accession: A55873  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-209 <SHA>  
 A:Cross-references: GB:U14752; NID:g681886; PIDN:AAA68520.1; PID:g681887  
 C:Superfamily: axon guidance signal protein  
 C:Keywords: lipoprotein; membrane protein

Query Match 31.4%; Score 342.5; DB 2; Length 209;  
 Best Local Similarity 42.5%; Pred. No. 5.8e-25;  
 Matches 90; Conservative 20; Mismatches 67; Indels 35; Gaps 10;

Qy 3 LPLPLRTVLMAAFGLSGPLRG-----GSSLRHVYVWNSNPRLL-----RGDAVVELG 49  
 Db 8 LPLPLLLLLL-----PLRARNEDPARANADRYAVYVWNSRPFQVSAGVGGGYTVEVS 60  
 Qy 50 LNDYLDVCPHYEGGPP-EGPETFALYVMDWPGYESQAGPRAYKRWC---SLRPGH 105  
 Db 61 INDYLDVCPHYGAPLPAERMEHYLYWNGEGHSCD-HRQGRFRWECNRPAAPGGP 119  
 Qy 106 VOFSEKIQRTFPFSLGFEFLPGETYYIYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHP 163  
 Db 120 LKFSKFLQFTFPFSLGFEFRPGHEYYIYISATPPNLDPRCLRLKVVYRPTNETIYEAPEP 179  
 Qy 164 VSGPESGTSWGRGDTPSPCLLLLLLLLLL 195  
 Db 180 IFT-SNNSCSGLGG-----CHLFTTVPVL 203

RESULT 7  
 A36377  
 B61 protein precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 29-Sep-1999  
 C:Accession: A36377  
 R:Holzman, L.B.; Marks, R.M.; Dixit, V.M.

Mol. Cell. Biol. 10, 5830-5838, 1990  
 A:Title: A novel immediate-early response gene of endothelium is induced by cytokines  
 A:Reference number: A36377; MUID:91042512  
 A:Accession: A36377  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-205 <HOL>  
 A:Cross-references: GB:M57730; GB:M37476; NID:g179320; PIDN:AAA58388.1; PID:g179321  
 C:Superfamily: axon guidance signal protein

Query Match 30.7%; Score 334.5; DB 2; Length 205;  
 Best Local Similarity 38.5%; Pred. No. 3.3e-24;  
 Matches 79; Conservative 27; Mismatches 72; Indels 27; Gaps 6;

Qy 11 LWAAFLGSLRGSSLRHVYVWNSNPRLLRGDAVVELGLNDYLDVCPHYEGGPPGPG 70  
 Db 4 LWAPLLGLCCSLAAADRTVFNWSSNPKRNEITYIHVOLNDYVDIICPHVEDHSDVADA 63  
 Qy 71 -ETFALYVMDWPGYESQAGPRAYKRWCSLP---FGHVQFSEKIQRTFPFSLGFEFLP 126  
 Db 64 MEQYILYLVEHEEYQLCPQS-KDOVRWQCNRPSSAKHGPEKLSKFKQRTFTPLTGKEFKE 122  
 Qy 127 GETYYIYISVPTPESSGQCLRLQVSVCCERKSESAHPVSGSGESTSWRGDTPS---- 182  
 Db 123 GHSYYIYISKPIHQHEDCLRLKVTYSGKITHSPQAHV--NPQEKRLA----ADDEPVRVL 176  
 Qy 183 -----PICLLLLLLLLLLL 195  
 Db 177 HSHGSAAPRLFPPLAWTVLLPLLL 201

RESULT 8  
 I49766  
 hepatoma transmembrane kinase ligand - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I49766  
 R:Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matth  
 Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995  
 A:Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine  
 A:Reference number: I49766; MUID:95199254  
 A:Accession: I49766  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-336 <RES>  
 A:Cross-references: GB:L38847; NID:g769677; PIDN:AAAC42052.1; PID:g769678  
 C:Genetics:  
 A:Gene: HTK

Query Match 15.1%; Score 164.5; DB 2; Length 336;  
 Best Local Similarity 29.9%; Pred. No. 6.6e-08;  
 Matches 55; Conservative 24; Mismatches 86; Indels 19; Gaps 6;

Qy 3 LPLPLRTVLMAAFGLSGPLRGSSLRHVYVWNSNPRLLRGDAV---ELGLNDYLDIVCP 59  
 Db 19 LMVLCRTAISRSIVLEP-----IYWNSSNKKFLPGQLVLYPQIG--DKLDIICP 66  
 Qy 60 HVEGPPGPPETTFALYVMDWPGYESQAGPRAYKRWCSLPFGHVQFSEKIQRTFPFS 119  
 Db 67 KVDSKTGQ-YEYKVVYVMDKQADRCTIKKENT-PLNCARPDDQDVKFTIKQEFSPNL 124  
 Qy 120 LGFEFLPGETYYIYISVPTPESSGQCLRLQVSVCCERKSESAHPVSGSGESTSWRGD 179  
 Db 125 WGLEFQKNKDYIIS--TSNGSLEGLDNQEGGVQCTRAMKILMKYGDQASSAGSARNHGP 182  
 Qy 180 TPSP 183  
 Db 183 TRRP 186

RESULT 9

## I84743

hepatoma transmembrane kinase ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999  
C:Accession: I84743  
R:Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews  
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995  
A:Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin  
A:Reference number: I49766; MUID:95199254  
A:Accession: I84743  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-333 <RES>  
A:Cross-references: GB:L38734; NID:9769675; PIDN:AAAC1752.1; PID:9769676  
C:Genetics:  
A:Gene: GDB:EPLG5; LERK5  
A:Cross-references: GDB:438338; OMIM:600527  
A:Map position: 13q33-13q33

Query Match 14.3%; Score 156; DB 2; Length 333;  
Best Local Similarity 28.9%; Pred. No. 4.2e-07;  
Matches 58; Conservative 27; Mismatches 78; Indels 38; Gaps 9;

QY 3 LLPLRTVLWAAFLGSLRGSSLRHVYWNSSNPRLLRGDAV---ELGLNDYLDIVCP 59

Db 16 LMVLCRTAISKSTVLEP-----IYWNSSNKFPLCQGLVLPQIG--DKLDIICP 63

QY 60 HYEGPGPEPETFALYVMDWPCYESQAEGRPRAYKRWVCSLPFGHVQSEKIQTPTFS 119

Db 64 KVDSKTVGQ-YEYKLYVMDWQDQADRTIKKENT-PLLNCAPQDQIKFTIKFQEFSPNL 121

QY 120 LGPEFLPGETYYIISVPTPESSGQCLRLQVSCCKERSAHPVG----SPG----- 168

Db 122 WGLEFQKNRDYIIS--TSNGSLEGLDNQEGGVCTFRAMKILMKVGQDASSAGSTRNKDP 179

QY 169 -----ESGTSGWRGGDTTSP 183

Db 180 TRRPELEAGTNG--RSSTTSP 198

## RESULT 10

## S46993

elk ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 15-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 28-May-1999  
C:Accession: S46993  
R:Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozl  
EMBO J. 13, 3757-3762, 1994  
A:Title: Molecular characterization of a family of ligands for eph-related tyrosine kin  
A:Reference number: S46993; MUID:94349923  
A:Accession: S46993  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-346 <REC>  
A:Cross-references: GB:U09304; NID:9538366; PIDN:AAA53093.1; PID:9538367

Query Match 13.4%; Score 146; DB 2; Length 346;  
Best Local Similarity 23.6%; Pred. No. 3.8e-06;  
Matches 61; Conservative 31; Mismatches 91; Indels 76; Gaps 10;

QY 6 LLRTVLWAAFLGSLRGSSLRHVYWNSSNPRLLRGDA-VVELGLNDYLDIVCPHYEG 63

Db 13 LVAMVWALCRLATPL---AKNLEPVSWSSLNPKFLSGKGLVYIPKIGDKLDIICPRAEA 69

QY 64 PGPEGPETFALYVMDWPCYESQAE-GPRAYKRWVCSLPFGHVQSEKIQTPTPSLGF 122

Db 70 GRP---YEYKLYLVPRPEQAACSTVLDPNVLV--TCNRPQEQIRFTIKFQEFSPNMG 124

QY 123 EFLLPGETYYIISVPTPESSGQCLRLQVSCCKERSAHPVG----- 165

Db 125 EFKKHHDYIITS--TSNGSLEGLNREGGVCTRTMKIIMKVGQDPNAVTPQDLTTSRPS 182

QY 166 -----SPGESGT-----SGWRGGDTTSP----- 183

Db 183 KEADNTVKMATQAPGSGILGSDGKHETVNOEKSGPGASGSGSDPDGFFFNKVALFA 242

QY 184 ----ICLLLLLLLLLILRL 198

Db 243 AVGAGCVIFLLIIFLTVL 261

## RESULT 11

## I58406

LERK-2 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I58406  
R:Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hol  
Oncogene 9, 3241-3248, 1994  
A:Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily con  
A:Reference number: I58406; MUID:95022634  
A:Accession: I58406  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-345 <RES>  
A:Cross-references: EMBL:U07560; NID:9563118; PIDN:AAAS3092.1; PID:9563119  
C:Genetics:  
A:Gene: Eplg2

Query Match 13.3%; Score 145; DB 2; Length 345;

Best Local Similarity 24.9%; Pred. No. 4.7e-06;

Matches 63; Conservative 27; Mismatches 89; Indels 74; Gaps 10;

QY 10 VLWAAFLGSLRGSSLRHVYWNSSNPRLLRGDA-VVELGLNDYLDIVCPHYEGPGPPE 68

Db 18 VLTCLRLATPL---AKNLEPVSWSSLNPKFLSGKGLVYIPKIGDKLDIICPRAEGRP-- 72

QY 69 GPETFALYVMDWPCYESQAE-GPRAYKRWVCSLPFGHVQSEKIQTPTPSLGFELPLG 127

Db 73 -YEYKLYLVPRPEQAACSTVLDPNVLV--TCNKPQEQIRFTIKFQEFSPNMGLEFKY 129

QY 128 EYIYIISVPTPESSGQCLRLQVSCCKER-----KSESAH 162

Db 130 HDYIITS--TSNGSLEGLNREGGVCTRTMKIIMKVGQDPNAVTPQDLTTSRPSKESDN 187

QY 163 PV-----GSPGES-----GTSGWRGGDTTSP-----C 185

Db 188 TVKTATQAPGSGILGSDGKHETVNOEKSGPGASGSGSDTDSFFNKSVALFAAVGAGC 247

QY 186 LLLLLLLLLLILRL 198

Db 248 VIFLLIIFLTVL 260

## RESULT 12

## I48780

Stral/Eplg2 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I48780; A55507; A55062; S52670  
R:Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaud, B.; Doll  
Dev. Biol. 170, 420-433, 1995  
A:Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in p19 embryona  
A:Reference number: I48780; MUID:95377533  
A:Accession: I48780  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-345 <RES>  
A:Cross-references: EMBL:Z48781; NID:9747858; PIDN:CAA88695.1; PID:9747859  
R:Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A  
Genomics 24, 127-132, 1994  
A:Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene enc  
A:Reference number: A55507; MUID:95203867

A:Accession: A55507  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-345 <FILE>  
 A:Cross-references: GB:U07598  
 R:Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.  
 J. Biol. Chem. 269, 26606-26609, 1994  
 A:Title: cDNA cloning and characterization of a ligand for the Cdk5 receptor protein-tyr  
 A:Reference number: A55062; MUID:95014510  
 A:Accession: A55062  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-89, T<sup>91</sup>-345 <SHA>  
 A:Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929  
 C:Genetics:  
 A:Gene: EPLG2

Query Match 13.2%; Score 144; DB 2; Length 345;  
 Best Local Similarity 24.5%; Pred. No. 5.9e-06;  
 Matches 62; Conservative 28; Mismatches 89; Indels 74; Gaps 10;

Qy 10 VLAAFLGSLRGSSLRHVYVWNSNRLRGDA-VVELGLNDYLDIVCPHYEGPGPPE 68  
 Db 18 VLTICRLATPL---AKNLEPVSWSLNPKFUSGKGLVYIPKIGDKLDIICPRAEAGRP-- 72  
 Qy 69 GPETALYMDWMPGYESCQAE-GPRAYKRWVCSLPFGHVQFSEKIQRTFTPSLGFELPG 127  
 Db 73 -YEYKLVLRPEQAACSTVLDPNVLV--TCNKHQEIERTIKQEFSPNWMGLEFKY 129  
 Qy 128 EYVYISVPTPESSGQCLRLQLVSVCKER-----KESAH 162  
 Db 130 HDYIITS--TSNGSLEGLNREGGVCRTRTKIVMKVGQDPNAVTPTEQLTTRSPKESDN 187  
 Qy 163 PV-----GSPGES-----GTSGRGGGTPSPPL-----C 185  
 Db 188 TVKTAQAPGRSGQSDGCKHETVNOEKSGPGAGGGGSDSPFNSKVALFAAVGAGC 247  
 Qy 186 LLLLLLLILRL 198  
 Db 248 VIFLLIIIFLVL 260

RESULT 13  
 T32645  
 hypothetical protein F56A11.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T32645  
 R:Gattung, S.; Goela, D.; Harper, M.  
 submitted to the EMBL Data Library, December 1997  
 A:Description: The sequence of C. elegans cosmid F56A11.  
 A:Reference number: 221204  
 A:Accession: T32645  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-462 <GAT>  
 A:Cross-references: EMBL:AF038619; PIDN:AA92075.1; GSPDB:GN00022; CESP:F56A11.3  
 A:Experimental source: strain Bristol N2; clone F56A11  
 C:Genetics:  
 A:Gene: CESP:F56A11.3  
 A:Map position: 4  
 A:Introns: 37/3; 69/2; 103/2; 220/1; 388/1; 412/3

Query Match 12.1%; Score 132.5; DB 2; Length 462;  
 Best Local Similarity 24.7%; Pred. No. 0.0001;  
 Matches 43; Conservative 27; Mismatches 55; Indels 49; Gaps 8;

Qy 28 HWYVNSNPNRLRGDAVVELGLNDYLDIVCPHYEGPGPPEFALYMDWMPGYESCQ 87  
 Db 93 HIVYWNSTNSLFRNQPTIEVRMGDVVRVCPDNE-EGRNDC-EYLLIYVETEFAMDDCA 150

Qy 88 AEGPRAYKRWV--CSLPFGHVQ-----FSEKIQRTFTPSL 120  
 Db 151 LE---SHSREVIRCA-PEGTAEKVLRTQOLSGRRREDKKQKPKVKNVAQLIQLNLPIN 206  
 Qy 121 GFEFLPGETYYIYISVPTPESSG-----QCLRLQVSVCKEKESAH 163  
 Db 207 GKQYQPGQTYIYMTSTGKANGTNHRMYGLCESQNMRLSMKV-----SASQPH 255  
 RESULT 14  
 T19914  
 hypothetical protein C43F9.8 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T19914  
 R:Mortimore, B.  
 submitted to the EMBL Data Library, November 1996  
 A:Reference number: Z19195  
 A:Accession: T19914  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-237 <WIL>  
 A:Cross-references: EMBL:Z82262; PIDN:CAB54195.1; GSPDB:GN00022; CESP:C43F9.8  
 A:Experimental source: clone C43F9  
 C:Genetics:  
 A:Gene: CESP:C43F9.8  
 A:Map position: 4  
 A:Introns: 32/2; 96/3; 214/1

Query Match 10.4%; Score 113; DB 2; Length 237;  
 Best Local Similarity 28.4%; Pred. No. 0.0032;  
 Matches 38; Conservative 16; Mismatches 62; Indels 18; Gaps 4;

Qy 3 LLPLRLTVLWAFGLGSLRGSSLRHVYVWNSNP--RLLRGDVAVELGLNDYLDIVCPH 60  
 Db 8 LLSLFPFIFGARKIPD-----INWISSNPIFDVSNTHDVHIGDRVSRICPK 56  
 Qy 61 YEGGPPGPEPTFALYMDWMPGYESCQAEGRPRAYKRWVCSLPFGHVQFSEKIQRTFTPSL 120  
 Db 57 SDETGK---YEYSIYVMSDEEYDCHFLSKPRLV--GACDNOTINASINIVRSFTPTPG 111

Qy 121 GFEFLPGETYYIIS 134  
 Db 112 GFEPQPGKNYFLIS 125

RESULT 15  
 I38000  
 Lutheran blood group glycoprotein precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 05-Nov-1999  
 C:Accession: I38000; S51663  
 R:Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houllihan, J.M.; Simpson, K.L.; Mawby, W.  
 Proc. Natl. Acad. Sci. U.S.A. 92, 5496-5500, 1995  
 A:Title: The Lutheran blood group glycoprotein, another member of the immunoglobulin  
 A:Reference number: I38000; MUID:95296337  
 A:Accession: I38000  
 A:Molecule type: mRNA  
 A:Residues: 1-628 <RES>  
 A:Cross-references: EMBL:X83425; NID:9603559; PIDN:CAA58449.1; PID:9603560  
 A:Note: parts of this sequence, including the amino end of the mature form, were conf  
 C:Genetics:  
 A:Gene: GDB:IJ  
 A:Cross-references: GDB:I20155; OMIM:111200  
 A:Map position: 19q12-19q13  
 C:Keywords: glycoprotein  
 F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:32-628/Product: Lutheran blood group glycoprotein #status experimental <MAT>

Query Match 8.0%; Score 87; DB 2; Length 628;  
 Best Local Similarity 28.7%; Pred. No. 2.9;



Result No.	Score	Query		ID	Description
		Match	Length		
1	1091	100.0	201	1	EFA4_HUMAN
2	898.5	82.4	206	1	EFA4_MOUSE
3	383.5	35.2	228	1	EFA5_MOUSE
4	383.5	35.2	228	1	EFA5_RAT
5	380.5	34.9	228	1	EFA5_HUMAN
6	376	34.5	195	1	EFA2_BRARE
7	373	34.2	228	1	EFA5_CHICK
8	365.5	33.5	228	1	EFA5_BRARE
9	364.5	33.4	238	1	EFA3_HUMAN
10	355	32.5	200	1	EFA2_CHICK
11	342.5	31.4	209	1	EFA2_MOUSE
12	340.5	31.2	213	1	EFA2_HUMAN
13	336.5	30.8	205	1	EFA1_MOUSE
14	334.5	30.7	205	1	EFA1_HUMAN
15	324.5	29.7	216	1	EFA1_XENLA
16	319.5	29.3	205	1	EFA1_RAT
17	296.5	27.2	187	1	EFA3_MOUSE
18	184	16.9	332	1	EFB2_BRARE
19	173.5	15.9	340	1	EFB3_MOUSE
20	169.5	15.5	340	1	EFB3_HUMAN
21	164.5	15.1	336	1	EFB2_MOUSE
22	156	14.3	327	1	EFB1_XENLA
23	156	14.3	333	1	EFB2_HUMAN
24	151	13.8	334	1	EFB1_CHICK
25	146	13.4	346	1	EFB1_HUMAN
26	145	13.3	345	1	EFB1_RAT
27	144	13.2	345	1	EFB1_MOUSE
28	88.5	8.1	1111	1	GLI1_HUMAN
29	87	8.0	628	1	LI1_HUMAN
30	84	7.7	382	1	CD34_MOUSE
31	83.5	7.7	378	1	MAT1_COCEL
32	83.5	7.7	577	1	VGLE_PVR1
33	82.5	7.6	198	1	RB16_RAT

```

DR InterPro: IPR001799; Ephrin.
DR Pfam: PF00812; Ephrin; 1.
DR PRINTS: PR01347; EPHRIN.
DR ProDom: PD002533; Ephrin; 1.
DR PROSITE: PS01299; EPHRIN; 1.
KW Glycoprotein; GPI-anchor; Signal; Alternative splicing.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 201 EPHRIN-A4.
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 157 201 KSESHPVSGSGTSGWGGTTPSPCLLLLLLLLRLL
FT LRL -> NLPSPKPESSQDLREESGLLPALGPQID
FT KME (IN SECRETED ISOFORM).
SQ SEQUENCE 201 AA; 22386 MW; 43501971DDIC6EA5 CRC64;

Query Match 100.0%; Score 1091; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.6e-94;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPLRLTVMWAFLGSPRGSSLRHVYVWNSNPRLLRGDAVVELGNDYLDIVCPH 60
DB 1 MRLPLRLTVMWAFLGSPRGSSLRHVYVWNSNPRLLRGDAVVELGNDYLDIVCPH 60
QY 61 YEGPGPEGPETFALYVMDWPGYSCQAEGRPRAYKRWVCSLPGHVQFSEKIQRTF 120
DB 61 YEGPGPEGPETFALYVMDWPGYSCQAEGRPRAYKRWVCSLPGHVQFSEKIQRTF 120
QY 121 GFELPGETYYIISVPTPESSGQCLRLQVSCCKERSAHPVSGSGTSGWGGDT 180
DB 121 GFELPGETYYIISVPTPESSGQCLRLQVSCCKERSAHPVSGSGTSGWGGDT 180
QY 181 PSLCLLLLLLLLLLLRLRL 201
DB 181 PSLCLLLLLLLLLLLRLRL 201

RESULT 2
ID EF44_MOUSE STANDARD; PRT; 206 AA.
AC O08542; O55218;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin-A4 precursor (EPH-related receptor tyrosine kinase ligand 4)
DE (LERK-4).
GN EFNA4 OR EPLG4 OR LERK4 OR EPL4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=98126446; PubMed=9465306;
RA Cerretti D.P., Nelson N.;
RT "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3), mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6): conservation of intron/exon structure.";
RL Genomics 47:131-135(1998).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC
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CC -----
DR EMBL: U90663; AAC50238.1; -.
DR EMBL: U92890; AAC39962.1; -.
DR EMBL: U92889; AAC39962.1; JOINED.
DR MGD: MGI:106643; Efn4.
DR InterPro: IPR001799; Ephrin.
DR Pfam: PF00812; Ephrin; 1.
DR PRINTS: PR01347; EPHRIN.
DR ProDom: PD002533; Ephrin; 1.
DR PROSITE: PS01299; EPHRIN; 1.
KW Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 206 EPHRIN-A4.
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC...) (POTENTIAL).
FT SITE 41 43 CELL ATTACHMENT SITE (POTENTIAL).
FT CONFLICT 1 4 MRL -> MLLRLGLIYPTPTPPAPGPLY (IN REF. 1).
SQ SEQUENCE 206 AA; 22861 MW; 43501971DDIC6EA5 CRC64;

Query Match 82.4%; Score 898.5; DB 1; Length 206;
Best Local Similarity 82.5%; Pred. No. 1.3e-76;
Matches 170; Conservative 9; Mismatches 22; Indels 5; Gaps 2;

QY 1 MRLPLRLTVMWAFLGSPRGSSLRHVYVWNSNPRLLRGDAVVELGNDYLDIVCPH 60
DB 1 MRLPLRLTVMWAFLGSPRGSSLRHVYVWNSNPRLLRGDAVVELGNDYLDIVCPH 60
QY 61 YEGPGPEGPETFALYVMDWPGYSCQAEGRPRAYKRWVCSLPGHVQFSEKIQRTF 117
DB 61 YEGPGPEGPETFALYVMDWPGYSCQAEGRPRAYKRWVCSLPGHVQFSEKIQRTF 120
QY 118 FSLGFELPGETYYIISVPTPESSGQCLRLQVSCCKERSKES--ESAHPVSGSGTSGW 175
DB 121 FPLGFELPGETYYIISVPTPESSGQCLRLQVSCCKERSGSHSAHPVSGSGTSGW 180
QY 176 RGDTPSPCLLLLLLLLLLLRLRL 201
DB 181 RGGHAPSPLCLLLLLLLLLLLRLRL 206

RESULT 3
ID EF45_MOUSE STANDARD; PRT; 228 AA.
AC O08543; O08544;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE (LERK-7) (AL-1).
GN EFNA5 OR EPLG7 OR LERK7 OR EPL7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=97060319; PubMed=8903354;
RA Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
RT "Distinct and overlapping expression patterns of ligands for Eph-related receptor tyrosine kinases during mouse embryogenesis.";
RL Dev. Biol. 179:382-401(1996).
CC -1- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION. INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE (BY SIMILARITY).
CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND

```



```

CC EPHB1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
CC IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
CC MICRODOMAINS (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC -----
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CC EMBL; U90664; AAB50239.1; -
CC DR EMBL; U90665; AAB50240.1; -
CC DR MGD; MGI:107444; Efnas.
CC DR InterPro; IPR001799; Ephrin.
CC DR Pfam; PF00812; Ephrin; 1.
CC DR PRINTS; PR01347; EPHRIN.
CC DR PRODOM; PD002533; Ephrin; 1.
CC DR PROSITE; PS01299; EPHRIN; 1.
CC KW Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
CC KW Alternative splicing.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT CHAIN 21 228 EPHRIN-A5.
CC FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARSPPLIC 163 189 MISSING (IN SHORT ISOFORM).
CC SQ SEQUENCE 228 AA; 26339 MW; 85439F5337420022 CRC64;
CC -----
Query Match 35.2%; Score 383.5; DB 1; Length 228;
Best Local Similarity 39.1%; Pred. No. 1.2e-28;
Matches 91; Conservative 31; Mismatches 70; Indels 41; Gaps 10;
QY 1 MRLPLRLTVLW-AAFLGSLRGSSSL---RHVVYWNSSNPRLLRGDVAVELGNDYLDI 56
   : ||| ||| ||| ||| : ||||| ||| ||| : ||| |||
Db 4 VEMLTLLFLVLMWCVFSQDP---GSKVADRYAYVWNSSNPRFQGDYHDVINCINDYLDV 60
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 57 VCPHVEGPGPEGPETALVMDWPGYESQAEGRAYKRWVCSLPF--GHVQFSEKIQ 113
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 FCPHYDSVPBDKTERVLVWNFEDGYSACD-HTSKGFKRWECNRHSPGPKFSEKQ 119
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 114 RFTFSLGFEFLPGETYYIYISVTPSSGQ-CLRLQSV-----CKK----- 154
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 LFTFSLGFEFPPGREFYIYSSAIPDNGRSCLKLVFVRTNSCMKTIGVHDRVFDVND 179
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 155 -----RKSESAPVSGPSGSGVNRGGTTPS-PLCLLLLLLLLLLLRLRLRI 200
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 180 KVENSELPADTVHESAEP-----SRGENAAQTPIPSRLAILLFLAMLTL 228
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
RESULT 4
EFAS_RAT STANDARD; PRT; 228 AA.
ID EFA5_RAT AC
AC P97605;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE (LERK-7) (AL-1).
DE GN EFNAS OR EPLG7 OR LERK7.
DE OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RA [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=95267434; Pubmed=7748564;
RA Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong S.C.,

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Best Local Similarity 38.5%; Pred. NO. 1.le-27;  
Matches 87; Conservative 29; Mismatches 84; Indels 26; Gaps

QY 1 MRLPLLRITVLAFLG-SPLRGSSLRHYVYWNSSNPRLLRGDAVVVELGNDYLDIVCP 59  
Db 4 VEMLLAAVALWCVRGCGPRKAVADRYAVYWNSTNPRFOQGDYHIDVCINDYLDVFCP 63  
QY 60 HYEGGPPGPEPTALYWDWPGVYESQAGPRAYKNWCSLFP---GHVQFSEKIQRTT 116  
Db 64 HYEDSVPEDKTERYVLVYVAFDGYSSCD-HISKGFKWECNRPHSPNGPLKFKSEKQLET 122  
QY 117 PFSGFFELPGCTEYVYTSVPTPESSGO-CLRLQVSV-----CCK-----E 155  
Db 123 PFSGFFEPGCEYFYISSAIPDNGRSCKLKVYVPANSCMKTGVDHVRVFDVNDKVE 182  
QY 156 RKSASAPVSPGSGTSGWRGGDTPSPCLCLLLLLLLLLLLLRLLRL 201  
Db 183 NSLEPADDTVRESAEPSPRGENAQTPRIPRILLATLLFLMLLLIL 228  
RESULT 8  
EFA5\_BRARE ID EFA5\_BRARE STANDARD; PRT; 228 AA.  
AC P79728;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Ephin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)  
DE (LERK-7) (AL-1) (ZEPH4L).  
GN EFN5 OR EFN5B OR AL1 OR EPLG7 OR LERK7.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Danio.  
ON NCBI\_TaxID=7955;  
OX [1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Embryo;  
RC MEDLINE=97195707; PubMed=9043080;  
RA Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,  
RA Bonhoeffer F., Holder N.;  
RT "Two Eph receptor tyrosine kinase ligands control axon growth and may  
RT be involved in the creation of the retinotectal map in the  
RT zebrafish.";  
RL Development 124:655-664(1997).  
CC -!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION  
CC OF THE RETINO-TECTAL MAP.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor  
CC (potential).  
CC -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.  
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF  
CC DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS  
CC STRONGLY EXPRESSED IN THE MIDBRAIN CAUDAL TO THE PRESUMPTIVE  
CC TECTUM. AT LATER STAGES IT IS MAINTAINED AT THE POSTERIOR MARGIN  
CC OF THE TECTUM.  
CC -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.  
CC  
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CC  
CC EMBL; Y09669; CAA70864.1; -.  
CC ZFIN; ZDB-GENE-980526-186; efna5b.  
CC InterPro; IPR001799; Ephrin.  
CC Pfam; PF00812; Ephrin.1.  
CC PRINTS; PR01347; EPHRIN.  
CC ProDom; PD002533; Ephrin.1.  
CC PROSITE; PS01299; EPHRIN; 1.  
CC Developmental protein. Neurogenesis. Glycoprotein; GPI-anchor. Signal  
CC KW

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FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 228 EPHRIN-A5.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 228 AA; 26595 MW; 74B3406C05418E6E CRC64;

Query Match 33.5%; Score 365.5; DB 1; Length 228;
Best Local Similarity 38.2%; Pred. No. 5.4e-27;
Matches 86; Conservative 33; Mismatches 75; Indels 31; Gaps 8;

QY 3 LPLLLRTVLW-AAFLGSPLRGSSLRHVYVWNSNPRLLRGDAVVELGLNDYLDIVCPHY 61
FT CHAIN 23 238 EPHRIN-A3.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 71 74 MISSING (IN REF. 2).
SQ SEQUENCE 238 AA; 26350 MW; 8EFD6AE8FE33FDDA CRC64;

Query Match 33.4%; Score 364.5; DB 1; Length 238;
Best Local Similarity 44.5%; Pred. No. 7.1e-27;
Matches 77; Conservative 16; Mismatches 67; Indels 13; Gaps 3;

QY 3 LPLLLRTVLW-AAFLGSPLRGSSLRHVYVWNSNPRLLRGDAVVELGLNDYLDIVCPHY 62
DB 8 LLLLVVPVLLPQLAQGGGALGNHRHAVVWNSNQHLLRREGYTVQVNVNDYLDIVCPHYN 67
QY 63 -----GPGPEGPETFALYVMDWPGYVESCQAEGRPRAYKRWCVS---LPEGHVQFSEK 111
DB 68 SSGVGPGAGPGGGAEQVLYVMSRNGYRTCNAS--QGFKWECNRPHAPHSPKFSK 125
QY 112 IORFPPFSLGFELPGETTYIVSVPTPSSGOCRLQVSVCCCKERKSESANHPV 164
DB 126 FQYSAFSLGYEFHAGHEYIYISTETHNLHMKLCRMKVFVCCASTSHSGKPV 178

RESULT 10
EFA3_HUMAN STANDARD; PRT; 238 AA.
AC P52797;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand 3)
DE (LEK-3) (EHK1 ligand) (EHK1-L).
GN EFNA3 OR EPLG3 OR LERK3 OR EFL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95140419; PubMed=7838529;
RA Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
RA Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
RA Cerretti D.P., Beckmann M.P.;
RT "Ligands for the receptor tyrosine kinases hek and elk: isolation of
RT cDNAs encoding a family of proteins.";
RL Oncogene 10:299-306(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95063919; PubMed=7973638;
RA Davis S., Gale N.W., Alarich T.H., Maisonnier P.C., Lhotak V.,
RA Pawson T., Goldfarb M., Yancopoulos G.D.;
RT "Ligands for EPH-related receptor tyrosine kinases that require
RT membrane attachment or clustering for activity.";
RL Science 266:816-819(1994).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKELETAL MUSCLE, SPLEEN,
CC THYMUS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE, AND PERIPHERAL
CC BLOOD LEUKOCYTES.
CC -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; U14187; AAC50078.1; -.
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DR EMBL; L37360; AAA52368.1; -.
DR MIM; 601381; -.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin.1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD02533; Ephrin.1.
DR PROSITE; PS01299; EPHRIN.1.
KW Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 238 EPHRIN-A3.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 71 74 MISSING (IN REF. 2).
SQ SEQUENCE 238 AA; 26350 MW; 8EFD6AE8FE33FDDA CRC64;

Query Match 33.4%; Score 364.5; DB 1; Length 238;
Best Local Similarity 44.5%; Pred. No. 7.1e-27;
Matches 77; Conservative 16; Mismatches 67; Indels 13; Gaps 3;

QY 3 LPLLLRTVLW-AAFLGSPLRGSSLRHVYVWNSNPRLLRGDAVVELGLNDYLDIVCPHY 62
DB 8 LLLLVVPVLLPQLAQGGGALGNHRHAVVWNSNQHLLRREGYTVQVNVNDYLDIVCPHYN 67
QY 63 -----GPGPEGPETFALYVMDWPGYVESCQAEGRPRAYKRWCVS---LPEGHVQFSEK 111
DB 68 SSGVGPGAGPGGGAEQVLYVMSRNGYRTCNAS--QGFKWECNRPHAPHSPKFSK 125
QY 112 IORFPPFSLGFELPGETTYIVSVPTPSSGOCRLQVSVCCCKERKSESANHPV 164
DB 126 FQYSAFSLGYEFHAGHEYIYISTETHNLHMKLCRMKVFVCCASTSHSGKPV 178

RESULT 10
EFA2_CHICK STANDARD; PRT; 200 AA.
AC P52802;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE (LEK-6) (ELF-1).
GN EFNA2 OR EPLG6 OR LERK6 OR ELF1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95360981; PubMed=7634327;
RA Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.;
RT "Complementary gradients in expression and binding of ELF-1 and Mek4
RT in development of the topographic retinotectal projection map.";
RL Cell 82:371-381(1995).
CC -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
CC EPHA5 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS THE TECTUM
CC BEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE.
CC -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; L40932; AAC42229.1; -.
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DR InterPro: IPR001799; Ephrin.
DR Pfam: PF00812; Ephrin; 1.
DR PRINTS: PR01347; EPHRIN.
DR PRODOM: PD002533; Ephrin; 1.
DR PROSITE: PS01299; EPHRIN; 1.
KW Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 200 EPHRIN-A2.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 200 AA; 23049 MW; 8FABIAE545ED96 CRC64;

Query Match 32.5%; Score 355; DB 1; Length 200;
Best Local Similarity 45.1%; Pred. No. 4.5e-26;
Matches 78; Conservative 22; Mismatches 63; Indels 10; Gaps 5;

QY 3 LLPLRLTVLWAAFLGSPGSLRHVVYVWSSNPRLLRGDAVVELGNDYLDVCPHYE 62
DB 10 LAIVGVCVNSDDPGKVI----SDRYAVYVWNRSPRFRHGDYTVESVINDYLDVCPHYE 65
QY 63 GPGPEGPEPTFALYVNDWDPGYESCAEGPRAYKRWCS---LPFGHVQFSEKIQRTTFFS 119
DB 66 EPLPAERMEYVLYVNYEGHASC-D-HRQKGPKEWNRDPSPGLKPFSEKFLTTPFS 124
QY 120 LGFEFLPGTYYIYISV-PTPESSGQCLRLQVSV-CCKERKSESAPVSGPSES 170
DB 125 LGFERPGHEYYIYISASPLNVVDRLCKLVYVVRTNDSLYESPFIITSNNS 177

RESULT 11
ID EFA2_MOUSE STANDARD; PRT; 209 AA.
AC P52801;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).
GN EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SWISS WEBSTER; TISSUE=Brain;
RX MEDLINE=95007776; PubMed=7522971;
RA Cheng H.J., Flanagan J.G.;
RT "Identification and cloning of ELF-1, a developmentally expressed
RT ligand for the Mek4 and Sek receptor tyrosine kinases.";
RL Cell 79:157-168(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95181289; PubMed=7876076;
RA Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit V.M.;
RT "cDNA cloning and characterization of a Cek7 receptor
RT protein-tyrosine kinase ligand that is identical to the ligand
RT (ELF-1) for the Mek4 and Sek receptor protein-tyrosine kinases.";
RL J. Biol. Chem. 270:3467-3470(1995).
CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
CC EPHA5.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (potential).
CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: U14941; AAA53636.1; -.
DR EMBL: U14752; AAA68520.1; -.
DR MGD: MGI:102707; Efn2.
DR InterPro: IPR001799; Ephrin.
DR Pfam: PF00812; Ephrin; 1.
DR PRINTS: PR01347; EPHRIN.
DR PRODOM: PD002533; Ephrin; 1.
DR PROSITE: PS01299; EPHRIN; 1.
KW Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 209 EPHRIN-A2.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 209 AA; 23586 MW; F1997545F25B9ABC CRC64;

Query Match 31.4%; Score 342.5; DB 1; Length 209;
Best Local Similarity 42.5%; Pred. No. 6.8e-25;
Matches 90; Conservative 20; Mismatches 67; Indels 35; Gaps 10;

QY 3 LLPLRLTVLWAAFLGSPGSLRHVVYVWSSNPRLLRGDAVVELGNDYLDVCPHYE 49
DB 8 LLPLRLTVLWAAFLGSPGSLRHVVYVWSSNPRLLRGDAVVELGNDYLDVCPHYE 60
QY 50 LNDYLDVCPHYEGCGPP-EGPETFALYVNDWDPGYESCAEGPRAYKRWVC---SLPFGH 105
DB 61 INDYLDIYCPHYGAPLPAERMEYVLYVNYEGHASC-D-HRQKGPKEWNRDPSPGLKPFSEKFLTTPFS 119
QY 106 VOFSEKIQRTTFFSGLGFEFLPGTYYIYISVPTPESSGQ-CLRLQVSV-CCKERKSESAPH 163
DB 120 LKFSKFLTTPFSGLGFEFLPGTYYIYISVPTPESSGQ-CLRLQVSV-CCKERKSESAPH 179
QY 164 VSGPESGTSWGRGDTSPGLCLLLLLLL 195
DB 180 IFT-SNSSCSGLGG-----CHLFTTTPVL 203

RESULT 12
ID EFA2_HUMAN STANDARD; PRT; 213 AA.
AC Q43921; O76020;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE (LERK-6) (HEK7-ligand) (HEK7-L).
GN EFNA2 OR EPLG6 OR LERK6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98126446; PubMed=9465306;
RA Cerretti D.P., Nelson N.;
RT "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
RT mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
RT conservation of intron/exon structure.";
RL Genomics 47:131-135(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Gordon J., Danganan L., Poundstone P.,
RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,
RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
```



Best Local Similarity 39.8%; Pred. No. 2.4e-24;  
Matches 80; Conservative 25; Mismatches 77; Indels 19; Gaps 5;

QY 11 LWAATFLGSPLRGGSLRHVVYVWSSNPRLRLRGDAVVLGNDLYDVCVHYEGPGPPEGP 70  
DDB 4 LWAPLGLCCSLAADRHHVFNWSSNPKFREEDYTVHVQLNDLYDIICPHVEDSDVAAA 63  
QY 71 -ETPVALYMDVMPQYESCQAEGRPRAYRKWVSLP---FGHVQFSEKIQRTPTPFSLGFELP 126  
DDB 64 MERYTLIYMEVHQEVACQPQS-KDQWRWNCNRPSAKHGPEKLSKFORFTPILGKEFKE 122  
QY 127 GETYYIYVPTPSSGQCLRLQVSCCKEKSSSAHPVSGPSES-----GTSG 174  
DDB 123 GHSYIYISKPIYHQESQCLKLTVNGKITHNPQAHV--NPQEKRLQADDPEQVVLHSIG 180  
QY 175 WRGGDTPSPCLCLLLLLLLLLL 195  
DDB 181 YSAAPRLFPLVWVLLPLLL 201

RESULT 14  
EFAL HUMAN  
ID EFAL HUMAN STANDARD; PRT; 205 AA.  
AC P20827;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-WAR-2002 (Rel. 41, Last annotation update)  
DE Ephrin-A1 precursor (EPH-related receptor tyrosine kinase ligand 1)  
DE (LERK-1) (Immediate early response protein B61) (Tumor necrosis  
DE factor, alpha-induced protein 4).  
GN EFNA1 OR EFGL1 OR LERK1 OR TNFAIP4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
[1]  
SEQUENCE FROM N.A.  
RP MEDLINE=91042512; PubMed=2233719;  
RP Holzman L.B., Marks R.M., Dixit V.M.;  
RA "A novel immediate-early response gene of endothelium is induced by  
RT cytokines and encodes a secreted protein.";  
RT Mol. Cell. Biol. 10:5830-5838(1990).  
RP [2]  
RP GPI-ANCHOR.  
RP MEDLINE=95140419; PubMed=7838529;  
RA Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,  
RA Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,  
RA Cerretti D.P., Beckmann M.P.;  
RA "Ligands for the receptor tyrosine kinases hek and elk: isolation of  
RT cDNAs encoding a family of proteins.";  
RT Oncogene 10:299-306(1995).  
CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,  
CC EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.  
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -1- INDUCTION: BY TNF-ALPHA AND INTERLEUKIN-1 BETA.  
CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DDB EMBL; M57730; AAA58388.1; -  
DDB PIR; A36377; A36377.  
DDB MIM; 191164; -  
DDB InterPro; IPR001799; Ephrin.  
DDB Pfam; PF00812; Ephrin; 1.  
DDB PRINTS; PD01347; EPHRIN.  
DDB PRODOM; PD002533; Ephrin; 1.  
DDB PROSITE; PS01299; EPHRIN; 1.

```

KW Glycoprotein; GPI-anchor: Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 205 EPHRIN-A1.
FT CARBOHYD 26 26 N-LINKED (GLCNAC...)(POTENTIAL).
SQ SEQUENCE 205 AA: 23771 MW: 4FEFC6BF4C1251A9 CRC64;

Query Match 30.7%; Score 334.5; DB 1; Length 205;
Best Local Similarity 38.5%; Pred. No. 3.7e-24;
Matches 79; Conservative 27; Mismatches 72; Indels 27; Gaps 6;

QY 11 LWAFLGSPRLGGSLRHVYVWNSNPRLLRGDAVVELGNDYLDIVCPHYEGPGPEGP 70
    ||| || : | : ||||| : | : ||||| : ||||| :
Db 4 LWAPLLGLCCSLAAADRHTVFVNSSNPKFRNEDYTIHVQLNDYVDIIICPHYEDSHVADAA 63

QY 71 -ETFALYWDVPWGYESCOAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTFSLGFEFLP 126
    ||| ||| : | : ||| : | : ||| : | : ||| : | : ||| : | : ||| :
Db 64 MEQYLILVHEEYQLCOPOS-KDVQRWCNRPSAKHGPEKLSEKFORTFTTLGKEFK 122

QY 127 GETYYISVTPESSGOCRLQVSCCKEKSESAHPVSGESGTSGWRGDTPS---- 182
    | : ||||| : | : ||||| : | : ||||| : | : ||||| : | : ||||| :
Db 123 GHSYYIISKPIQHEDCLRLKVTYSGKITHSPOAHV--NPQEKRLA-----ADDPVRVL 176

QY 183 -----PLCLLLLLLLLLL 195
    || : ||| : |
Db 177 HSIHSAAPRLFPLAWTVLLPLL 201

RESULT 15
EFAL_XENLA STANDARD; PRT; 216 AA.
AC A52794;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin-A1 precursor (EPH-related receptor tyrosine kinase ligand 1)
DE (LERK-1) (XELF).
GN EFNA1 OR EPGL1 OR ELF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipelidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RX NCBI
RN R00000
RP SEQUENCE FROM N.A.
RX MEDLINE=97000306; PubMed=8843391;
RA Weinstein D.C., Rahman S.M., Ruiz J.C., Hemmati-Briavanlou A.;
RT "Embryonic expression of eph signalling factors in Xenopus.";
RL Mech. Dev. 57:133-144(1996).
CC C-1 SUBUNIT BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
CC EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHAL (BY
CC SIMILARITY).
CC C-1 SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC C-1 SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U31204; AAA74485.1; -.
CC EMBL; U31205; AAA74486.1; -.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Glycoprotein; GPI-anchor; Alternative splicing; Signal.
FT SIGNAL 1 28 POTENTIAL.
```

FT CHAIN 29 216 EPHRIN-A1.  
FT CARBOHYD 36 36 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT VARSPPLIC 162 216 TTPPVNVHTPRSHIQSDEPEVPLPGVMKSVAGNSAAPGTPC  
SQ SEQUENCE 216 AA; 24755 MW; 1B3A508E0A7B872E CRC64;  
TLYGLLAALLLRL -> SE (IN ISOFORM A').

Query Match 29.7%; Score 324.5; DB 1; Length 216;  
Best Local Similarity 39.7%; Pred. No. 3.3e-23;  
Matches 83; Conservative 25; Mismatches 66; Indels 35; Gaps 9;

QY 11 LWAAFLGSLRGSSLRHVWVWSSNPRLLRGDAVVELGNDYLDIVCPHY-EGPGPEG 69  
DB 21 LW-----LREAQGERHIVFWSSNTRFMQEDTVQVQLNDYLDIVCPYEEGSGVAGHT 73  
QY 70 PETFALYVMDWPGYESQAGPRAYKRWGSLPF--GHVQFSEKIQRTFPFSLGFEFLP 126  
DB 74 VERTFLVDYEEYETCKPKS-KDOVWECNKPFPAPHCPEKCEKFKFTFTFLGTETFE 132  
QY 127 GETYYIISVTPPESSGQCLRLQVSVCK-----ERKSESAHP-VGSPG-----ES 170  
DB 133 GRTYYIISKPIYHGETCMRLRVHVSGRTPPPVNVHTPRSHIQSDEPEVPLPGVMKVA 192  
QY 171 GTSWRGGDTPSPCLL--LLLLLLILRL 197  
DB 193 GNSA-----APGTPCTLYGLLAALLLRL 216

Search completed: September 28, 2002, 01:48:25  
Job time: 639 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 28, 2002, 01:47:36 ; Search time 79.86 Seconds  
(without alignments)  
435.412 Million cell updates/sec

Title: US-09-904-954-4  
Perfect score: 1091  
Sequence: 1 MRLPLRLTVLNAFLGSP.....SPICLLLLLLLLLRLLRL 201

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*

- 1: sp-archaea:\*
- 2: sp-bacteria:\*
- 3: sp-fungi:\*
- 4: sp-human:\*
- 5: sp-invertebrate:\*
- 6: sp-mammal:\*
- 7: sp-mhnc:\*
- 8: sp-organelle:\*
- 9: sp-phage:\*
- 10: sp-plant:\*
- 11: sp-rodent:\*
- 12: sp-virus:\*
- 13: sp-vertebrate:\*
- 14: sp-unclassified:\*
- 15: sp-xvirus:\*
- 16: sp-bacteriap:\*
- 17: sp-archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	891.5	81.7	206	11	Q9CZS8	Q9CZS8 mus musculus
2	480	44.0	202	13	Q98TZ1	Q98TZ1 gallus gall
3	329.5	30.2	205	11	Q9D7K8	Q9D7K8 mus musculus
4	320.5	29.4	229	13	Q93431	Q93431 brachydanio
5	315	28.9	219	13	Q90YC5	Q90YC5 brachydanio
6	267.5	24.5	102	11	Q9WUE7	Q9WUE7 rattus norv
7	263.5	24.2	118	11	Q923G4	Q923G4 rattus norv
8	217.5	19.9	88	13	Q9PTD0	Q9PTD0 ctenophorus
9	212	19.4	93	13	Q9PTD1	Q9PTD1 ctenophorus
10	188	17.2	80	13	Q42304	Q42304 brachydanio
11	169.5	15.5	333	13	Q9PUJ4	Q9PUJ4 gallus gall
12	167	15.3	334	13	Q90Z32	Q90Z32 brachydanio
13	158.5	14.5	652	5	Q9V4E1	Q9V4E1 drosophila
14	153	14.0	279	5	Q9U474	Q9U474 caenorhabdi
15	144.5	13.2	341	13	Q90Z33	Q90Z33 brachydanio
16	137.5	12.6	331	13	Q90Z31	Q90Z31 brachydanio

17	132.5	12.1	348	5	O44516	O44516 caenorhabdi
18	130.5	12.0	327	13	Q9PT69	Q9PT69 xenopus lae
19	113	10.4	237	5	Q9U3M2	Q9U3M2 caenorhabdi
20	94.5	8.7	729	5	Q9ULK9	Q9ULK9 drosophila
21	93.5	8.6	2322	4	Q92675	Q92675 homo sapien
22	88.5	8.1	577	12	Q9Q3F7	Q9Q3F7 pseudorabie
23	85.5	7.8	1793	5	Q9W451	Q9W451 drosophila
24	85	7.8	164	16	Q9AB51	Q9AB51 caulobacter
25	85	7.8	268	2	Q02303	Q02303 pseudomonas
26	83.5	7.7	558	12	Q9LHR5	Q9LHR5 pseudorabie
27	83.5	7.7	578	12	Q9PYC0	Q9PYC0 pseudorabie
28	83.5	7.7	741	5	Q9W4X5	Q9W4X5 drosophila
29	83	7.6	555	12	Q9LHR4	Q9LHR4 pseudorabie
30	83	7.6	594	4	O94865	O94865 homo sapien
31	83	7.6	932	4	Q9H196	Q9H196 homo sapien
32	83	7.6	932	4	Q9NT26	Q9NT26 homo sapien
33	82	7.5	206	10	O48787	O48787 arabidopsis
34	82	7.5	474	13	O73906	O73906 gallus gall
35	82	7.5	935	4	Q96L35	Q96L35 homo sapien
36	82	7.5	1017	4	O9HCF6	O9HCF6 homo sapien
37	80.5	7.4	505	2	Q9RKL2	Q9RKL2 streptomyce
38	80	7.3	756	4	O43304	O43304 homo sapien
39	79	7.2	278	17	Q9HQL8	Q9HQL8 halobacteri
40	78.5	7.2	527	6	Q9MYK7	Q9MYK7 trichosurus
41	78	7.1	277	11	Q9D571	Q9D571 mus musculu
42	78	7.1	620	12	Q98329	Q98329 molluscum c
43	78	7.1	970	4	Q9P107	Q9P107 homo sapien
44	78	7.1	993	11	O35902	O35902 mus musculu
45	77.5	7.1	248	16	O32232	O32232 bacillus su

#### ALIGNMENTS

RESULT 1

Q9CZS8 ID Q9CZS8 PRELIMINARY; PRT; 206 AA.  
AC Q9CZS8;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE 10 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,  
DE CLONE:2610529M21, FULL INSERT SEQUENCE.  
GN EFNA4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,  
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK012195; BAB28092.1; -.

```
DR MGD; MGI:106643; Efn4.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
SQ SEQUENCE 206 AA; 22859 MW; 675E32971D1C6EBC CRC64;

Query Match 81.7%; Score 891.5; DB 11; Length 206;
Best Local Similarity 81.6%; Pred. No. 4.3e-83;
Matches 168; Conservative 11; Mismatches 22; Indels 5; Gaps 2;

QY 1 MRLPLRLTVMWAAFLGSLRGGSSLRHVYWNSSNPRLLRGDAVVELGLNDYDVCVPH 60
DB 1 MRLPLRLTVMWAAFLGSLRPGCSSLRHPIYWNSSNPRLLRGDAVVELGNDYDVCVPH 60

QY 61 YEGGPEPETFALYVMDWPGYESQAGPRAYKRWVCSL---PFGHVQFSEKIQRTFP 117
DB 61 YESPGPEPETFALYVMDWPGYESQAGPRAYKRWVCSL---PFGHVQFSEKIQRTFP 120

QY 118 FSLGFELPGCTYYTISVPTPESSGQCLRLQVSVCCCKERS--ESAHVPGSPGESGTSGW 175
DB 121 FPLGFELPGCTYYTISVPTPESSGQCLRLQVSVCCCKERS--ESAHVPGSPGESGTSGW 180

QY 176 RGGDTPSPCLLLLLLLLLLILRLIL 201
DB 181 RGGHAPSPLCLLLLLLLLLLILRLVL 206

RESULT 2
Q98T21 PRELIMINARY; PRT; 202 AA.
AC Q98T21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE EPHRIN-A6 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP Menzel P., Valencia F., Godement P., Dodelet V.C., Pasquale E.B.;
RT "Ephrin-A6, a new ligand for EphA receptors in the developing visual
system.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF317286; AAK00944.1; -.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
FT NON_TER
SQ SEQUENCE 202 AA; 22624 MW; 91E2716FF91353F9 CRC64;

Query Match 44.0%; Score 480; DB 13; Length 202;
Best Local Similarity 51.9%; Pred. No. 4e-41;
Matches 97; Conservative 22; Mismatches 56; Indels 12; Gaps 4;

QY 6 LLRTVLWAAFLGSLRGGSSLRHVYWNSSNPRLLRGDAVVELGLNDYDVCVPHYEGPG 65
DB 1 LLGELLWAPLLWAPPVVRGRHGVYANGSNPRFLQDDYSIQVSIINDHLDIYCPHSAPT 60

QY 66 PPEGPETFALYVMDWPGYESQAGPRAYKRWVCSLPGF---HVQFSEKIQRTFPFSLGF 122
DB 61 P--WAESETLFMVDDEGYRC--SETPGAKRWCNKPFPAPFVPVRESEKIQRTFPFSLGF 117

QY 123 EFLPGCTYYTISVPTPESSGQCLRLQVSVCCCKERS-----SAHPVPGSPGESGTSGWR 176
DB 123 EFLPGCTYYTISVPTPESSGQCLRLQVSVCCCKERS-----SAHPVPGSPGESGTSGWR 176

Db 118 EFRPGETYYTISVPTPESSGQCLRLKRVSVCCRASTPEPLTEVPNSQPRGGGPEGAGSP 177
QY 177 GGDTPSP 183
DB 178 RDAAPIP 184

RESULT 3
Q9D7K8 PRELIMINARY; PRT; 205 AA.
AC Q9D7K8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ADULT MALE TONGUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:2310004J15, FULL INSERT SEQUENCE.
GN EFNA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casanova T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AK009144; BAB26102.1; -.
DR MGD; MGI:103236; Efnal.
DR InterPro; IPR001799; Ephrin.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
SQ SEQUENCE 205 AA; 23772 MW; E37E55767459A4EC CRC64;

Query Match 30.2%; Score 329.5; DB 11; Length 205;
Best Local Similarity 39.3%; Pred. No. 9.2e-26;
Matches 79; Conservative 25; Mismatches 78; Indels 19; Gaps 5;

QY 11 LWAFLGSLRGGSSLRHVYWNSSNPRLLRGDAVVELGLNDYDVCVPHYEGPGPEGP 70
DB 4 LWAFLGSLRGGSSLRHVYWNSSNPKFREEDYTHVQLNDYDVCVPHYEGPVADAA 63

QY 71 -ETFALYVMDWPGYESQAGPRAYKRWVCSLP---FGHVQFSEKIQRTFPFSLGFELP 126
DB 64 MERYTILMYHEQYVACQPOS-KDQVRWNCNRPASAKHGPEKLSVKFQRTFPFLGKEFKE 122

QY 127 GETYYTISVPTPESSGQCLRLQVSVCCCKERSAHPVPGSPGES-----GTSG 174
DB 123 GHSYYTISKPIYHQSQCCLKVTVNGKITHNPQAHV--NPQEKRLQADPEVQVLSHG 180

QY 175 WRGGDTPSPCLLLLLLLLLLIL 195
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RESULT	5		
Q90YC5			
ID	Q90YC5	PRELIMINARY;	PRT; 219 AA.
AC	Q90YC5;		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
DE	EPHRIN-A3.		
DE	EPHRIN-A3.		
GN	Brachydanio rerio (zebrafish) (Zebra danio),		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
OC	Cypriniformes; Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
OX	NCBI_TaxID=7955;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=21412237; PubMed=11520665;		
RA	Hirate Y., Miseda M., Harada T., Yamasu K., Okamoto H.;		
RT	"Identification of ephrin-A3 and novel genes specific to the midbrain-		
RT	MHB in embryonic zebrafish by ordered differential display.";		
RL	Mech. Dev. 107:83-96(2001).		
RL	EMBL; AB051678; BAB5891.1.		

	Query Match	24.5%	Score 267.5	DB 11	Length 102
	Best Local Similarity	55.7%	Pred. No. 8.4e-20		
	Matches 54	Conservative 9	Mismatches 29	Indels 5	Gaps 3
QY	46	VEIGLNDYLDIVCPHYEGPQP-EGPTFFALYMDVPGYESCQEGPRAYKRWVC	---	SL 101	
		:                :      :     :      :			
Db	3	VEVSINDYLDIYPHYGAPLPPAERMERYILYMYNGEGHSCD-HRQGFRRWCNRPAA	61		
QY	102	PFQHVQSEKIQRTFSLGFEFLPGETYYIVSPTP	138		
		:			
Db	62	PGGLKPESEKFOFLTPESLGFEFRPGHYEYISATPP	98		

RESULT	7	
Q923G4		
ID	Q923G4	PRELIMINARY; PRT; 118 AA.
AC	Q923G4;	
DT	01-DEC-2001	(TREMBLrel. 19, Created)
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)
DE	EPHRIN A3 (FRAGMENT).	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata;	Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia;	Sciurognathi; Muridae; Rattus.

```

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Munoz J.J., Alonso-C L.M., Sacedon R., Crompton T., Vicente A.,
RT Jimenez E., Varas A., Zapata A.G.;
RT "Expression and function of the Eph A receptors and their ligands
RL ephrins A in the rat thymus.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY045577; AAK92219.1; -
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13470 MW; FF0277F079783A46 CRC64;

Query Match 24.2%; Score 263.5; DB 11; Length 118;
Best Local Similarity 43.3%; Pred. No. 2.6e-19;
Matches 52; Conservative 16; Mismatches 47; Indels 5; Gaps 2;

QY 58 CPHEGPGPEPTFALYMDVPGVSCQAEGRAYKRWVCS---LPFGHVQFSEKIQIR 114
DB 1 CPHYSSGPGGAQVLYVNLGSGYRTCNAS--QGSKRWCNRQHASHSPIKSEKFOR 58
QY 115 FPPFSLGFEFLDGETYYIVSVTPESPSSGQCLRLQVSCCKERKSESAAHPVGPSPGSGTSG 174
DB 59 YSAFSLGYEFHAGQEYYIISTPTNHLHWKLRMKVFCVCCASKDFEGENQVPKLEKSISG 118

RESULT 8
Q9PTD0 PRELIMINARY; PRT; 88 AA.
AC Q9PTD0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EPHRIN A3 (FRAGMENT).
OS Ctenophorus ornatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC Ctenophorus.
OX NCBI_TaxID=95347;
RN [1]
RP SEQUENCE FROM N.A.
RA Scarbrough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
RT "Ephrin homologs are expressed in the adult lizard visual system.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF209777; AAF19444.1; -
DR InterPro: IPR001799; Ephrin.
DR Pfam: PF00812; Ephrin; 1.
DR ProDom: PD002533; Ephrin; 1.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 10636 MW; C56FCD8B13F219E7 CRC64;

Query Match 19.9%; Score 217.5; DB 13; Length 88;
Best Local Similarity 45.6%; Pred. No. 8.9e-15;
Matches 41; Conservative 13; Mismatches 31; Indels 5; Gaps 2;

QY 30 VYWNSSNPRLRGDAVVELGLNDYDIVCPHYEGPGPGPETFALYMDVDPGYESQAE 89
DB 1 VFWNRNPNLRREGYTVQSVNDYLDYICPHYNASVPEGRVQYILYMYNVEGYRTCNIS 60
QY 90 GPRAYKRWVCS---LPFGHVQFSEKIQRT 116
DB 61 --QGFKRWECNRPHAPHSPIKSEKFOR 88

Query Match 19.4%; Score 212; DB 13; Length 93;
Best Local Similarity 45.6%; Pred. No. 3.5e-14;
Matches 41; Conservative 16; Mismatches 29; Indels 4; Gaps 2;

QY 30 VYWNSSNPRLRGDAVVELGLNDYDIVCPHYEGPGPGPETFALYMDVDPGYESQAE 89
DB 1 VFCNRSNPRFWOGEYTVAVSINDYLDYICPYYESQPHSRMERYILFMVNHGDLTCE-H 59
QY 90 GPRAYKRWVCS---LPFGHVQFSEKIQRT 116
DB 60 RMRGFKRWECNRQSPDPGLRFESEKFOR 89

RESULT 10
Q42304 PRELIMINARY; PRT; 80 AA.
AC Q42304;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EPHRIN-A5 (FRAGMENT).
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MacDonald R., Scholes J., Strahle U., Brennan C., Holder N., Brand M.,
RA Wilson S.;
RT "The Pax protein Noi protein is required for commissural axon pathway
RL formation in the rostral forebrain.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12928; CAA73391.1; -
DR ZFIN; ZDB-GENE-001128-1; efna5a.
DR InterPro: IPR001799; Ephrin.
DR Pfam: PF00812; Ephrin; 1.
DR ProDom: PD002533; Ephrin; 1.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 9674 MW; 712DDC6058214993 CRC64;

Query Match 17.2%; Score 188; DB 13; Length 80;

```

Best Local Similarity 45.6%; Pred. No. 8.1e-12;  
Matches 36; Conservative 13; Mismatches 26; Indels 4; Gaps 2;

QY 41 RGDVVELGLNDYLDIVCPHYEGPGPEGFALYMDWPCYSCQAGPRAYRWKCS 100  
DB 3 RGDYHIDVINDYLDVCPHYMDVTPERTERYLYMVNYDGYSSCD-HTAKGFARWECN 61

QY 101 LPF---GHVQFSEKIQRT 116  
DB 62 RPHSPNGPLKFEKQLEFT 80

RESULT 11  
Q9PUJ4 ID Q9PUJ4 PRELIMINARY; PRT; 333 AA.  
AC Q9PUJ4;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)  
DE EPHRIN-B2 PRECURSOR.  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Menzel P., Pasquale E.B.;  
RT "Coding sequence of chicken ephrin-B2";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF180729; AAD53948.1;  
DR InterPro; IPR001799; Ephrin.  
DR Pfam; PF00812; Ephrin; 1.  
DR ProDom; PD002533; Ephrin; 1.  
DR PROSITE; PS01299; Ephrin; 1.  
KW SIGNAL.  
FT SIGNAL 1 27 POTENTIAL.  
FT CHAIN 28 333 EPHRIN-B2.  
SQ SEQUENCE 333 AA; 36761 MW; 4C28E8CB211B7783 CRC64;

Query Match 15.5%; Score 169.5; DB 13; Length 333;  
Best Local Similarity 25.7%; Pred. No. 3.5e-09;  
Matches 64; Conservative 33; Mismatches 81; Indels 71; Gaps 10;

QY 3 LPLPLRTVLWAFGLSPRGSSLRHVYWNSSNPLRLRGDAV---ELGLNDYLDIVCP 59  
DB 18 LMLVRLTALAKSIVLDP-----IYWNSSNPKFLPGGGLVLYPQIG--DKLIDTICP 65

QY 60 HYECPGPEPETFALYMDWPCYSCQAGPRAYRWKCSLPFGHVQFSEKIQRTTFFS 119  
DB 66 KYDSKTVGQ-YEYKYVWVDKQADSCAIRKNDT-PLNCAKPDQDVFTIKFQFSPNL 123

QY 120 LGFEFLPGTYYIISVPTPESSGQCLQVSVCCERKESAHVPV---SPG----- 168  
DB 124 WGLEQKNDYVIS--TSNGSLEGLNQGEGVCQTKMKILMKVQDPNSAGLPRSTD 181

QY 169 -----ESCTSWRGDTPSP- 189  
DB 182 TKRPEQAGTNG--KSSTTSPFVKDHSSTGDSKAGHSSILGSEVALFAGIASGCIIFI 239

QY 190 LLLILRL 198  
DB 240 VIIITLV 248

RESULT 12  
Q90Z32 ID Q90Z32 PRELIMINARY; PRT; 334 AA.  
AC Q90Z32;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)

DE EPHRIN B2B.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21290827; PubMed=11397014;  
RA Chan J., Mabiy J.D., Serluca F.C., Chen J.N., Goldstein N.B.,  
RA Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;  
RT "Morphogenesis of prechordal plate and notochord requires intact  
ephrin b signaling";  
RL Dev. Biol. 234:470-482(2001).  
DR EMBL; AF375226; AAK64276.1;  
SQ SEQUENCE 334 AA; 36998 MW; 341497E0FE9473BD CRC64;

Query Match 15.3%; Score 167; DB 13; Length 334;  
Best Local Similarity 27.4%; Pred. No. 6.3e-09;  
Matches 64; Conservative 30; Mismatches 76; Indels 64; Gaps 11;

QY 24 SSLRHWVWNSNPLRLRGDAV---ELGLNDYLDIVCPHYEGPGPE--GPETALYMW 78  
DB 24 STVLESIYWNSTKVFVPGVGVLYPQIG--DKMDIVCPRIK-PGSTEQTNIYEYRVYLV 80

QY 79 DWPGVYSCQAGPRAYRWK---CSLPFGHVQFSEKIQRTTFFSGLFPEFLPGTYYIS 134  
DB 81 PREQLETCVHT-----KSDMLLLNCDDQDVKFTKQFSPNLWGLEFLRGKDYHIS 135

QY 135 VPTP-----ESSGQC-----LRLQVSVCCERKESAHVPVSP----- 167  
DB 136 TSNSTFEGLNDHNGVGVCRSKMKLVLRVQSPDTSFSAKNHPTRNPPKYPENKQNTFSK 195

QY 168 -----GES-GTSGWGRGDTPTPLCLL-----LLLLLLILRLRL 201  
DB 196 ENDVSQIDSMQNGESGGKSGSVGSAGSDVALFAGVAGAVIFILLIIVALL 249

RESULT 13  
Q9V4EI ID Q9V4EI PRELIMINARY; PRT; 652 AA.  
AC Q9V4EI;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)  
DE EPHRIN PROTEIN.  
GN EPHRIN OR CG1862.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Dai Y., Kunes S.;  
RT "Isolation and Characterization of Drosophila Ephrin";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Gloddek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
DR EMBL: AF216287; AAF28394.1; -;  
DR EMBL: AE003843; AAF59335.2; -;  
DR FlyBase: FBgn040324; Ephrin.  
DR InterPro: IPR001799; Ephrin.  
DR Pfam: PF00812; Ephrin; 1.  
DR ProDom: PD002533; Ephrin; 1.  
SQ SEQUENCE 652 AA; 72302 MW; 5BA2F02F15964594 CRC64;

Query Match 14.5%; Score 158.5; DB 5; Length 652;  
Best Local Similarity 30.6%; Pred. No. 1e-07;  
Matches 44; Conservative 25; Mismatches 52; Indels 23; Gaps 8;  
QY 30 VYVNSSNP--RLRGDAVVELGLN-----DYLDIVCPHYEGPGPEG-PETFALYMDVW 80  
DB 219 MHWNTSNTFRINDTHIDVKNGLAFEDQVHICPVIE-PGTENETEKIIVNSK 277  
QY 81 PGYESQAEQ--PRAYKRWVCSLPFGHVQFSEKIQRTPFSLGFEFLPGETYYIIVSPTP 138  
DB 278 VEYETCRITNADPRVIA--ICDKPQIMFEITIFRFTPTQPGGLEFLPGNDYFIISTSK 335  
QY 139 ES-----SQQC-----LRLQVSVCC 153  
DB 336 DDLRYRRIGRCSTNNKMKVFKVCC 359

RESULT 14  
ID Q90474 PRELIMINARY; PRT; 279 AA.  
AC Q90474;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE VAB-2 (HYPOTHETICAL PROTEIN Y37E11AR.6).  
GN VAB-2 OR Y37E11AR.6.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N2;  
RX MEDLINE=20084449; PubMed=10619431;  
RA Chin-Sang I.D., George S.E., Ding M., Moseley S.L., Lynch A.S.,  
RA Chisholm A.D.;  
RT "The ephrin VAB-2/EFN-1 functions in neuronal signaling to regulate

RT epidermal morphogenesis in *C. elegans*.";  
RL Cell 99:781-790(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode *C. elegans*: a platform for  
RT investigating biology. The *C. elegans* Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Miller N., Maggi L.;  
RT "The sequence of *C. elegans* cosmid Y37E11AR.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Waterston R.;  
RT "Direct Submission.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF201079; AAF25647.1; -;  
DR EMBL: AC024759; AAK68436.1; -;  
DR InterPro: IPR001799; Ephrin.  
DR Pfam: PF00812; Ephrin; 1.  
DR ProDom: PD002533; Ephrin; 1.  
SQ SEQUENCE 279 AA; 32068 MW; 8C291A92D97D39EF CRC64;

Query Match 14.0%; Score 153; DB 5; Length 279;  
Best Local Similarity 28.9%; Pred. No. 1.4e-07;  
Matches 41; Conservative 21; Mismatches 72; Indels 8; Gaps 4;  
QY 30 VYVNSSNPRLRGDAVVELGLNDIVCPHYEGPGPEGPFETALYMDVWPCYESQAE 89  
DB 28 IWNSTNPLIVERAAI-----GDTLDIVCPFD-ENSEDELTEQSIYRVTEEYENCER 81  
QY 90 GPRAYKRWVCSLPFGHVQFSEKIQRTPFSLGFEFLPGETYYIIVSPTPESGQCRLQV 149  
DB 82 S-KAKELGRCTQYQEKLVAFRLMSPNPSGLDYPGVYFISTSTGSRKG-LYNEQG 139  
QY 150 SVCCERKESAHVPGSPGESG 171  
DB 140 GLCASHNLKMWIHTORNGDIG 161

RESULT 15  
ID Q90233 PRELIMINARY; PRT; 341 AA.  
AC Q90233;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE EPHRIN B1.  
OS Brachydanio rerio (zebrafish) (zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21290827; PubMed=11397014;  
RA Chan J., Mabry J.D., Serluca F.C., Chen J.N., Goldstein N.B.,  
RA Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;  
RT "Morphogenesis of prechordal plate and notochord requires intact  
RL eph/ephrin b signaling.";  
RL Dev. Biol. 234:470-482(2001).  
DR EMBL: AF375224; AAK64274.1; -;  
SQ SEQUENCE 341 AA; 37849 MW; CB922F20E0D93E94 CRC64;

Query Match 13.2%; Score 144.5; DB 13; Length 341;

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Best Local Similarity 25.7%; Pred. No. 1.3e-06;
Matches 65; Conservative 26; Mismatches 89; Indels 73; Gaps 13;

Qy 11 LW--AATLGSPLRGSSLRHVVYWNSSNPRLLRGDAVV--ELGLNDYLDIVCPHYEGPG 65
Db 12 LWILTAMCRYALPAAKSLESVV-WNSQNPKFVSGKGLVIYPEIG--DKLDIICPKGDMGR 68

Qy 66 PPEGPEFALYVMDWPGYESCOA-EGPRAYKRWGCSLPFGHVQFSEKIQRTFPFSLGFEEF 124
Db 69 P---YEFYKLYLVKKEAESCSTILDPNVLV--TCNKPEKDIKFTIKFQEFSPNYMGLFEF 123

Qy 125 LPGETYYIISVP--TPE-----SSGQCLRLQVSVCCCKERKSESA----- 161
Db 124 KRFTNYIITSTNGTQEGLENREGVCSTRSMKILMKVQDPNAPDPDLPLDRPYDNE 183

Qy 162 --HPVGSPG-----ESGTSGRGGDT-----PSPL-----C 185
Db 184 IKDPTTSRKRTERGENEVGNGSKMPGKDTNRNONSFGSVEGIFGSKPALFAAIGAGC 243

Qy 186 LLLLLLLLRLL 198
Db 244 VIFLLIIIIILVL 256
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